Table 3.

AA800738	13145			Null					Homo sapiens, clone IMAGE:4179558		rc_AA800738 EST190235 Rattus norvegicus cDNA, 3' end /clone=RLUAK86 /clone_end=3' /gb=AA800738 /gi=2863693 /ug=Rn.6629 /len=581
AA800763	13146			Null					EST(not recognised)		rc_AA800763 EST190260 Rattus norvegicus cDNA, 3' end /clone=RLUAL17 /clone_end=3' /gb=AA800763 /gi=2863718 /ug=Rn.6636 /len=475
AA800800	13147			Null					EST (not recognized)		rc_AA800800 EST190297 Rattus norvegicus cDNA, 3' end /clone=RLUAL59 /clone_end=3' /gb=AA800800 /gi=2863755 /ug=Rn.1945 /len=550
AA800882	13148			Null					Mus musculus 11 days embryo head cDNA, RIKEN		rc_AA800882 EST190379 Rattus norvegicus cDNA, 3' end /clone=RLUAM60 /clone_end=3' /gb=AA800882 /gi=2863837 /ug=Rn.24136 /len=379
AA817685	13149	NP_071581	13150	XM_048473		XP_048473		88	Cytochrome b5	NM_022245	rc_AA817685 UI-R-A0-aa-b-12-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-A0-aa-b-12-0-UI /clone_end=3' /gb=AA817685 /gi=2887565 /ug=Rn.1055 /len=399
AA818604	13151	NP_114177	13152	M11717	13153	AAA52697	13154	87	Heat shock protein 70-1 (Hspa1a	NM_031971	rc_AA818604 UI-R-A0-bc-h-02-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-A0-bc-h-02-0-UI /clone_end=3' /gb=AA818604 /gi=2889343 /ug=Rn.1950 /len=516
AA819643	13155			Null					EST (not recognized)		rc_AA819643 UI-R-A0-an-f-10-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-A0-an-f-10-0-UI /clone_end=3' /gb=AA819643 /gi=2888907 /ug=Rn.2277 /len=568

Table 3.

AA849036	13156	NP_058786	13157	NM_000856	13158	NP_000847	13159	80	guanylate cyclase 1, soluble, alpha 3 (Gucy1a3),	NM_017090	rc_AA849036 EST191798 Rattus norvegicus cDNA, 3' end /clone=RLUAJ79 /clone_end=3' /gb=AA849036 /gi=2936576 /ug=Rn.1974 /len=629
AA852046	13160			Null					ovarian cathepsin B amplicon	AF057143	rc_AA852046 EST194815 Rattus norvegicus cDNA, 3' end /clone=RSPAP85 /clone_end=3' /gb=AA852046 /gi=2939586 /ug=Rn.11350 /len=424
AA858641	13161			Null					EST (not recognized)		rc_AA858641 UI-R-E0-bq-d-09-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-bq-d-09-0-UI /clone_end=3' /gb=AA858641 /gi=2948981 /ug=Rn.16559 /len=542
AA859468	13162			Null					EST (not recognized)		UI-R-E0-bv-e-04-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-bv-e-04-0-UI /clone_end=3' /gb=AA859468 /gi=2948988 /ug=Rn.226 /len=434
AA859835	13163			Null					EST(not recognised)		rc_AA859835 UI-R-E0-cc-g-07-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-cc-g-07-0-UI /clone_end=3' /gb=AA859835 /gi=2949355 /ug=Rn.784 /len=418
AA859835	13164			Null					EST(not recognised)		rc_AA859835 UI-R-E0-cc-g-07-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-cc-g-07-0-UI /clone_end=3' /gb=AA859835 /gi=2949355 /ug=Rn.784 /len=418
AA859922	13165			Null							rc_AA859922 UI-R-E0-cg-c-04-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-cg-c-04-0-UI /clone_end=3' /gb=AA859922 /gi=2949442 /ug=Rn.819 /len=373
AA859966	13166			Null					Strong homology with 18S rRNA (V01270)		UI-R-E0-ca-g-03-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-ca-g-03-0-UI /clone_end=3' /gb=AA859966 /gi=2949486 /ug=Rn.861 /len=392

Table 3.

AA859996	13167			Null					Homo sapiens cDNA: FLJ23343 fis, clone HEP13562		rc_AA859996 UI-R-E0-ca-b-04-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-ca-b-04-0-UI /clone_end=3' /gb=AA859996 /gi=2949516 /ug=Rn.22634 /len=553
AA866248	13168	BAA07197	13169	NM_006452	13170	NP_006443	13171	96	Rat AIRC mRNA for AIR carboxylase-SAICAR synthetase, complete cds	D37979	UI-R-A0-bg-h-03-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-A0-bg-h-03-0-UI /clone_end=3' /gb=AA866248 /gi=2981694 /ug=Rn.3015 /len=557
AA866485	13172			Null					EST (not recognized)		rc_AA866485 UI-R-A0-bd-e-03-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-A0-bd-e-03-0-UI /clone_end=3' /gb=AA866485 /gi=2981697 /ug=Rn.3018 /len=406
AA874887	13173	CAA06377	13174	AB019987	13175	BAA73535	13176	100	ESTs, Weakly similar to SMC-protein [R.norvegicus]		rc_AA874887 UI-R-E0-ci-g-10-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-ci-g-10-0-UI /clone_end=3' /gb=AA874887 /gi=2979835 /ug=Rn.3162 /len=478
AA874887	13177	CAA06377	13178	AB019987	13179	BAA73535	13180	100	ESTs, Weakly similar to SMC-protein [R.norvegicus]		UI-R-E0-ci-g-10-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-ci-g-10-0-UI /clone_end=3' /gb=AA874887 /gi=2979835 /ug=Rn.3162 /len=478
AA874918	13181	AAC39971	13182	NM_003899	13183	NP_003890	13184	86	PAK-interacting exchange factor beta-PIX	AF044673	rc_AA874918 UI-R-E0-ck-g-08-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-ck-g-08-0-UI /clone_end=3' /gb=AA874918 /gi=2979866 /ug=Rn.10963 /len=519

Table 3.

AA875045	13185	NP_032827	13186	NM_002601	13187	NP_002592	13188	89n	phosphodiesterase 6D, cGMP-specific, rod, delta		rc_AA875045 UI-R-E0-cb-c-03-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-cb-c-03-0-UI /clone_end=3' /gb=AA875045 /gi=2979993 /ug=Rn.3214 /len=543
AA875060	13189			Null					EST (not recognized)		UI-R-E0-cb-f-05-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-cb-f-05-0-UI /clone_end=3' /gb=AA875060 /gi=2980008 /ug=Rn.3225 /len=548
AA875136	13190			Null					EST(not recognised)		rc_AA875136 UI-R-E0-bu-f-02-0-UI.s2 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-bu-f-02-0-UI /clone_end=3' /gb=AA875136 /gi=2980084 /ug=Rn.2804 /len=581
AA875186	13191			Null					Mus musculus adult male colon cDNA, RIKEN		rc_AA875186 UI-R-E0-ce-h-05-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-ce-h-05-0-UI /clone_end=3' /gb=AA875186 /gi=2980134 /ug=Rn.3753 /len=403
AA875291	13192	NP_058756	13193	NM_007069	13194	NP_009000	13195	78	Hras-revertant gene 107	NM_017060	rc_AA875291 UI-R-E0-cn-e-02-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-cn-e-02-0-UI /clone_end=3' /gb=AA875291 /gi=2980239 /ug=Rn.11377 /len=323
AA875438	13196			Null					Mus musculus adult male tongue cDNA, RIKEN		rc_AA875438 UI-R-E0-cs-h-12-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-cs-h-12-0-UI /clone_end=3' /gb=AA875438 /gi=2980386 /ug=Rn.24931 /len=563
AA875563	13197	NP_033083	13198	XM_054015		XP_054015		89n	Mus musculus reticulocalbin (Rcn)	NM_009037	rc_AA875563 UI-R-E0-cm-b-06-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-cm-b-06-0-UI /clone_end=3' /gb=AA875563 /gi=2980511 /ug=Rn.3275 /len=472

Table 3.

AA875635	13199			Null					EST (not recognized)		rc_AA875635 UI-R-E0-ct-f-05-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-ct-f-05-0-UI /clone_end=3' /gb=AA875635 /gi=2980583 /ug=Rn.2984 /len=367
AA891037	13200	R5RT3L	13201	U65581	13202	Q92901	13203	95	ESTs, Moderately similar to 60S RIBOSOMAL PROTEIN L3 [R.norvegicus]		rc_AA891037 EST194840 Rattus norvegicus cDNA, 3' end /clone=RHEAO17 /clone_end=3' /gb=AA891037 /gi=3017916 /ug=Rn.16548 /len=401
AA891242	13204	AAB31016	13205	XM_004995		XP_004995		89n	Myosin light chain-2 isoform	S70785	rc_AA891242 EST195045 Rattus norvegicus cDNA, 3' end /clone=RHEAQ93 /clone_end=3' /gb=AA891242 /gi=3018121 /ug=Rn.3843 /len=559
AA891242	13206	AAB31016	13207	XM_004995		XP_004995		89n	Myosin light chain-2 isoform	S70785	rc_AA891242 EST195045 Rattus norvegicus cDNA, 3' end /clone=RHEAQ93 /clone_end=3' /gb=AA891242 /gi=3018121 /ug=Rn.3843 /len=559
AA891438	13208	AAF23952	13209	XM_045474	13210	XP_045474	13211	94n	Mus musculus pantothenate kinase 1 beta (panK1beta)	AF200357	rc_AA891438 EST195241 Rattus norvegicus cDNA, 3' end /clone=RHEAU25 /clone_end=3' /gb=AA891438 /gi=3018317 /ug=Rn.22406 /len=397
AA891438	13212	AAF23952	13213	XM_045474	13214	XP_045474	13215	94n	Mus musculus pantothenate kinase 1 beta (panK1beta)	AF200357	rc_AA891438 EST195241 Rattus norvegicus cDNA, 3' end /clone=RHEAU25 /clone_end=3' /gb=AA891438 /gi=3018317 /ug=Rn.22406 /len=397

Table 3.

AA891651	13216			Null					EST (not recognized)		rc_AA891651 EST195454 Rattus norvegicus cDNA, 3' end /clone=RKIAF13 /clone_end=3' /gb=AA891651 /gi=3018530 /ug=Rn.1318 /len=499
AA891689	13217	AF161380	13218	AAF28940	13219			89n	HSPC262		rc_AA891689 EST195492 Rattus norvegicus cDNA, 3' end /clone=RKIAF57 /clone_end=3' /gb=AA891689 /gi=3018568 /ug=Rn.14704 /len=421
AA891727	13220	XM_042640		XP_042640				92n	EST (hypothetical protein)		EST195530 Rattus norvegicus cDNA, 3' end /clone=RKIAG04 /clone_end=3' /gb=AA891727 /gi=3018606 /ug=Rn.3418 /len=418
AA891828	13221	BC014026	13222	AAH14026	13223			88n	Homo sapiens, Similar to RAD23		rc_AA891828 EST195631 Rattus norvegicus cDNA, 3' end /clone=RKIAH33 /clone_end=3' /gb=AA891828 /gi=3018707 /ug=Rn.6963 /len=546
AA891828	13224	AAD41775	13225	XM_029247		XP_029247		63	Procollagen, type I, alpha 2	AF121217	rc_AA891828 EST195631 Rattus norvegicus cDNA, 3' end /clone=RKIAH33 /clone_end=3' /gb=AA891828 /gi=3018707 /ug=Rn.6963 /len=546
AA891857	13226	AAD40012	13227	NM_012192	13228	NP_036324	13229	92	Rattus norvegicus small zinc finger-like protein (TIM9b)	AF150106	rc_AA891857 EST195660 Rattus norvegicus cDNA, 3' end /clone=RKIAH77 /clone_end=3' /gb=AA891857 /gi=3018736 /ug=Rn.13451 /len=501
AA891943	13230			Null					EST (not recognized)		rc_AA891943 EST195746 Rattus norvegicus cDNA, 3' end /clone=RKIAI86 /clone_end=3' /gb=AA891943 /gi=3018822 /ug=Rn.3564 /len=550

Table 3.

AA892012	13231	XNRTDM	13232	M22632	13233	XNHUDM	13234	94	Glutamate oxaloacetate transaminase 2, mitochondrial (aspartate aminotransferase 2)	rc_AA892012 EST195815 Rattus norvegicus cDNA, 3' end /clone=RKIAK66 /clone_end=3' /gb=AA892012 /gi=3018891 /ug=Rn.3628 /len=363
AA892012	13235	XNRTDM	13236	M22632	13237	XNHUDM	13238	94	Glutamate oxaloacetate transaminase 2, mitochondrial (aspartate aminotransferase 2)	EST195815 Rattus norvegicus cDNA, 3' end /clone=RKIAK66 /clone_end=3' /gb=AA892012 /gi=3018891 /ug=Rn.3628 /len=363
AA892154	13239	NP_037292	13240	NM_006454	13241	NP_006445	13242	50	Mad4 homolog (human)	rc_AA892154 EST195957 Rattus norvegicus cDNA, 3' end /clone=RKIAN02 /clone_end=3' /gb=AA892154 /gi=3019033 /ug=Rn.3279 /len=386
AA892154	13243	NP_037292	13244	NM_006454	13245	NP_006445	13246	50	Mad4 homolog (human)	rc_AA892154 EST195957 Rattus norvegicus cDNA, 3' end /clone=RKIAN02 /clone_end=3' /gb=AA892154 /gi=3019033 /ug=Rn.3279 /len=386
AA892228	13247	NP_071568	13248	NM_006260	13249	NP_006251	13250	86	Protein-kinase, interferon-inducible double stranded RNA dependent inhibitor	rc_AA892228 EST196031 Rattus norvegicus cDNA, 3' end /clone=RKIAN91 /clone_end=3' /gb=AA892228 /gi=3019107 /ug=Rn.4183 /len=459

Table 3.

AA892228	13251	NM_006260	13252	NP_006251	13253			86	Protein-kinase, interferon-inducible double stranded RNA dependent inhibitor	EST196031 Rattus norvegicus cDNA, 3' end /clone=RKIAN91 /clone_end=3' /gb=AA892228 /gi=3019107 /ug=Rn.4183 /len=459
AA892468	13254	P27435	13255	L41351	13256	Q16651	13257	76	Rattus norvegicus mRNA for prostasin precursor, complete cds	rc_AA892468 EST196271 Rattus norvegicus cDNA, 3' end /clone=RKIAQ80 /clone_end=3' /gb=AA892468 /gi=3019347 /ug=Rn.22724 /len=474
AA892468	13258	P27435	13259	L41351	13260	Q16651	13261	76	Rattus norvegicus mRNA for prostasin precursor, complete cds	rc_AA892468 EST196271 Rattus norvegicus cDNA, 3' end /clone=RKIAQ80 /clone_end=3' /gb=AA892468 /gi=3019347 /ug=Rn.22724 /len=474
AA892551	13262			Null					EST	rc_AA892551 EST196354 Rattus norvegicus cDNA, 3' end /clone=RKIAS76 /clone_end=3' /gb=AA892551 /gi=3019430 /ug=Rn.14765 /len=112
AA892551	13263			Null					EST	rc_AA892551 EST196354 Rattus norvegicus cDNA, 3' end /clone=RKIAS76 /clone_end=3' /gb=AA892551 /gi=3019430 /ug=Rn.14765 /len=112
AA892635	13264	TVRTRH	13265	M31470	13266	TVHUC4	13267	99	Ras-like protein	rc_AA892635 EST196438 Rattus norvegicus cDNA, 3' end /clone=RKIAV15 /clone_end=3' /gb=AA892635 /gi=3019514 /ug=Rn.12720 /len=478

Table 3.

AA892635	13268	TVRTRH	13269	M31470	13270	TVHUC4	13271	99	Ras-like protein		EST196438 Rattus norvegicus cDNA, 3' end /clone=RKIAV15 /clone_end=3' /gb=AA892635 /gi=3019514 /ug=Rn.12720 /len=478
AA892805	13272			Null					Mus musculus adult male testis cDNA, RIKEN		rc_AA892805 EST196608 Rattus norvegicus cDNA, 3' end /clone=RKIAX50 /clone_end=3' /gb=AA892805 /gi=3019684 /ug=Rn.19944 /len=499
AA892817	13273			Null					EST (not recognized)		rc_AA892817 EST196620 Rattus norvegicus cDNA, 3' end /clone=RKIAX62 /clone_end=3' /gb=AA892817 /gi=3019696 /ug=Rn.14794 /len=650
AA892855	13274	NP_033099	13275	XM_006049		XP_006049		64(mus)	ESTs, Highly similar to ROM1 MOUSE ROD OUTER SEGMENT MEMBRANE PROTEIN 1 [M.musculus]	NM_009073	rc_AA892855 EST196658 Rattus norvegicus cDNA, 3' end /clone=RKIAY14 /clone_end=3' /gb=AA892855 /gi=3019734 /ug=Rn.14796 /len=532
AA892888	13276			Null					EST (not recognized)		rc_AA892888 EST196691 Rattus norvegicus cDNA, 3' end /clone=RKIAY54 /clone_end=3' /gb=AA892888 /gi=3019767 /ug=Rn.14801 /len=508
AA892919	13277	AAA41719	13278			Null		No Human	Nucleolar phosphoprotein of 140kD	M94288	rc_AA892919 EST196722 Rattus norvegicus cDNA, 3' end /clone=RKIAY91 /clone_end=3' /gb=AA892919 /gi=3019798 /ug=Rn.9517 /len=574

Table 3.

AA892919	13279	AAA41719	13280	XM_005918		XP_005918		42	nucleolar phosphoprotein of 140kD, Nopp140	M94288	rc_AA892919 EST196722 Rattus norvegicus cDNA, 3' end /clone=RKIAY91 /clone_end=3' /gb=AA892919 /gi=3019798 /ug=Rn.9517 /len=574
AA892942	13281			Null					EST (not recognized)		rc_AA892942 EST196745 Rattus norvegicus cDNA, 3' end /clone=RKIBA19 /clone_end=3' /gb=AA892942 /gi=3019821 /ug=Rn.3611 /len=511
AA893158	13282	AAA37238	13283	NM_001156	13284	NP_001147	13285	88	synexin	L13129	rc_AA893158 EST196961 Rattus norvegicus cDNA, 3' end /clone=RKIBC88 /clone_end=3' /gb=AA893158 /gi=3020037 /ug=Rn.18916 /len=428
AA893191	13286			Null					EST(not recognised)		rc_AA893191 EST196994 Rattus norvegicus cDNA, 3' end /clone=RKIBD35 /clone_end=3' /gb=AA893191 /gi=3020070 /ug=Rn.3301 /len=654
AA893191	13287			Null					EST(not recognised)		rc_AA893191 EST196994 Rattus norvegicus cDNA, 3' end /clone=RKIBD35 /clone_end=3' /gb=AA893191 /gi=3020070 /ug=Rn.3301 /len=654
AA893210	13288	O35142	13289	X70476	13290	P35606	13291	97	Beta prime COP		EST197013 Rattus norvegicus cDNA, 3' end /clone=RKIBD55 /clone_end=3' /gb=AA893210 /gi=3020089 /ug=Rn.11141 /len=608
AA893212	13292			Null					EST (Limited homology to thioredoxin reductase gene, partial cds)		rc_AA893212 EST197015 Rattus norvegicus cDNA, 3' end /clone=RKIBD58 /clone_end=3' /gb=AA893212 /gi=3020091 /ug=Rn.23943 /len=638

Table 3.

AA893275	13293	XM_048457	13294	XP_048457	13295			87n	Homo sapiens KIAA0892 protein		rc_AA893275 EST197078 Rattus norvegicus cDNA, 3' end /clone=RKIBE38 /clone_end=3' /gb=AA893275 /gi=3020154 /ug=Rn.22748 /len=505
AA893325	13296	NP_071986	13297	NM_000274	13298	NP_000265	13299	87	ornithine aminotransferase (Oat)	NM_022521	rc_AA893325 EST197128 Rattus norvegicus cDNA, 3' end /clone=RKIBF09 /clone_end=3' /gb=AA893325 /gi=3020204 /ug=Rn.1430 /len=464
AA893552	13300	AAB39509	13301	NM_006215	13302	NP_006206	13303	53	Rattus norvegicus kallistatin mRNA, complete cds	U51017	rc_AA893552 EST197355 Rattus norvegicus cDNA, 3' end /clone=RLIAD83 /clone_end=3' /gb=AA893552 /gi=3020431 /ug=Rn.11152 /len=669
AA893596	13304	AK016067	13305	BC003542	13306	AAH03542	13307	93(mus)	Mouse RIKEN full-length cDNA		rc_AA893596 EST197399 Rattus norvegicus cDNA, 3' end /clone=RPLAC38 /clone_end=3' /gb=AA893596 /gi=3020475 /ug=Rn.22237 /len=564
AA893596	13308	AK016067	13309	BC003542	13310	AAH03542	13311	93(mus)	Mouse RIKEN full-length cDNA		EST197399 Rattus norvegicus cDNA, 3' end /clone=RPLAC38 /clone_end=3' /gb=AA893596 /gi=3020475 /ug=Rn.22237 /len=564
AA893602	13312	BAA88213	13313	NM_022461	13314	NP_071906	13315	81	Mus musculus AZ2 mRNA	AB007141	rc_AA893602 EST197405 Rattus norvegicus cDNA, 3' end /clone=RPLAC44 /clone_end=3' /gb=AA893602 /gi=3020481 /ug=Rn.14812 /len=567

Table 3.

AA893671	13316	Q63244	13317	U02310	13318	1923399A	13319	93	ESTs, Weakly similar to HFH1 RAT HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 1 [R.norvegicus]		rc_AA893671 EST197474 Rattus norvegicus cDNA, 3' end /clone=RPLAI27 /clone_end=3' /gb=AA893671 /gi=3020550 /ug=Rn.22754 /len=399
AA893690	13320	NP_062308	13321	BC010665	13322	AAH10665	13323	86n	Mus musculus neuronal protein 15.6 (Np15.6-pending)	NM_019435	rc_AA893690 EST197493 Rattus norvegicus cDNA, 3' end /clone=RPLAI47 /clone_end=3' /gb=AA893690 /gi=3020569 /ug=Rn.3377 /len=492
AA893885	13324			Null					EST (not recognized)		rc_AA893885 EST197688 Rattus norvegicus cDNA, 3' end /clone=RPLAN11 /clone_end=3' /gb=AA893885 /gi=3020764 /ug=Rn.3719 /len=392
AA893939	13325	NP_033195	13326	XM_044488		XP_044488		92n	Mus musculus split hand/foot deleted gene 1	NM_009169	rc_AA893939 EST197742 Rattus norvegicus cDNA, 3' end /clone=RPLAN70 /clone_end=3' /gb=AA893939 /gi=3020818 /ug=Rn.8472 /len=416
AA893985	13327			Null					EST (rare)		EST197788 Rattus norvegicus cDNA, 3' end /clone=RPLAO24 /clone_end=3' /gb=AA893985 /gi=3020864 /ug=Rn.14842 /len=400
AA894004	13328	NP_031625	13329	BC000728	13330	AAH00728	13331	87n	Mus musculus, Similar to capping protein (actin filament)	NM_007599	rc_AA894004 EST197807 Rattus norvegicus cDNA, 3' end /clone=RPLAO48 /clone_end=3' /gb=AA894004 /gi=3020883 /ug=Rn.8945 /len=430

Table 3.

AA894232	13332			Null					EST (not recognized)		rc_AA894232 EST198035 Rattus norvegicus cDNA, 3' end /clone=RSPAT41 /clone_end=3' /gb=AA894232 /gi=3021111 /ug=Rn.13522 /len=485
AA894297	13333			Null					EST(not recognised)		rc_AA894297 EST198100 Rattus norvegicus cDNA, 3' end /clone=RSPAW18 /clone_end=3' /gb=AA894297 /gi=3021176 /ug=Rn.3510 /len=554
AA926149	13334	NP_036652	13335	NM_001752	13336	NP_001743	13337	88	Catalase	NM_012520	rc_AA926149 UI-R-A1-eq-h-04-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-A1-eq-h-04-0-UI /clone_end=3' /gb=AA926149 /gi=3073285 /ug=Rn.3001 /len=449
AA944177	13338	NP_037095	13339	X12597	13340	P09429	13341	94	High mobility group 1 (Hmg1)		rc_AA944177 EST199676 Rattus norvegicus cDNA, 3' end /clone=REMAD31 /clone_end=3' /gb=AA944177 /gi=3104093 /ug=Rn.4121 /len=596
AA945573	13342	NP_058854	13343	NM_000769	13344	NP_000760	13345	72	Cytochrome P450, 2c39	NM_017158	EST201072 Rattus norvegicus cDNA, 3' end /clone=RLIAP18 /clone_end=3' /gb=AA945573 /ug=Rn.1247 /len=651
AA946292	13346	NP_037286	13347	NM_005195	13348	NP_005186	13349	81	CCAAT/enhancerbinding, protein (C/EBP) delta	NM_013154	EST201791 Rattus norvegicus cDNA, 3' end /clone=RLUBD38 /clone_end=3' /gb=AA946292 /ug=Rn.6975 /len=468
AA955167	13350	NP_032564	13351	XM_039759		XP_039759		84n	Mus musculus myristoylated alanine rich protein kinase C substrate	NM_008538	rc_AA955167 UI-R-A1-du-a-08-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-A1-du-a-08-0-UI /clone_end=3' /gb=AA955167 /ug=Rn.9560 /len=443

Table 3.

AA955477	13352	CAA54183	13353	BC010407	13354	AAH10407	13355	88n	ESTs, Moderately similar to S78100 MAPK-activated protein kinase (EC 2.7.1.-) 2 - mouse (fragment) [M.musculus]		rc_AA955477 UI-R-A1-ex-f-01-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-A1-ex-f-01-0-UI /clone_end=3' /gb=AA955477 /ug=Rn.8789 /len=394
AA963674	13356	NP_058941	13357	XM_009189		XP_009189		96	Rattus norvegicus eukaryotic translation elongation factor 2	NM_017245	rc_AA963674 UI-R-E1-gg-h-01-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E1-gg-h-01-0-UI /clone_end=3' /gb=AA963674 /ug=Rn.7194 /len=333
AA963674	13358	NP_058941	13359	XM_009189		XP_009189		96	Rattus norvegicus eukaryotic translation elongation factor 2	NM_017245	rc_AA963674 UI-R-E1-gg-h-01-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E1-gg-h-01-0-UI /clone_end=3' /gb=AA963674 /ug=Rn.7194 /len=333
AA998882	13360	NP_074060	13361	XM_005918		XP_005918		42	nucleolar phosphoprotein p130 (Nopp140	NM_022869	rc_AA998882 UI-R-C0-hp-a-11-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-C0-hp-a-11-0-UI /clone_end=3' /gb=AA998882 /ug=Rn.9517 /len=478
AI009098	13362	BC004560	13363	AAH04560	13364			92n	Similar to oxygen regulated protein (150kD)		EST203549 Rattus norvegicus cDNA, 3' end /clone=REMBI58 /clone_end=3' /gb=AI009098 /ug=Rn.983 /len=549
AI009111	13365	NP_058974	13366	NM_002786	13367	NP_002777	13368	97	Proteasome (prosome, macropain) subunit, alpha type 1	NM_017278	rc_AI009111 EST203562 Rattus norvegicus cDNA, 3' end /clone=REMBI74 /clone_end=3' /gb=AI009111 /ug=Rn.2668 /len=612

Table 3.

AI010357	13369	NP_068534	13370	NM_006667	13371	NP_006658	13372	79	25-Dx protein (25Dx	NM_021766	rc_AI010357 EST204808 Rattus norvegicus cDNA, 3' end /clone=RLUBX66 /clone_end=3' /gb=AI010357 /ug=Rn.4232 /len=754
AI013795	13373	NP_073204	13374	NM_003241	13375	NP_003232	13376	52	Dorsal protein 1	NM_022713	rc_AI013795 EST208470 Rattus norvegicus cDNA, 3' end /clone=RSPBS90 /clone_end=3' /gb=AI013795 /ug=Rn.9984 /len=246
AI045558	13377	JE0155		AF041254	13378	O43615	13379	90	Translocator of inner mitochondrial membrane 44		rc_AI045558 UI-R-C1-jz-h-03-0-UI.s2 Rattus norvegicus cDNA, 3' end /clone=UI-R-C1-jz-h-03-0-UI /clone_end=3' /gb=AI045558 /ug=Rn.10801 /len=422
AI045558	13380	JE0155		XM_049282	13381	XP_049282	13382	90	Translocator of inner mitochondrial membrane 44		UI-R-C1-jz-h-03-0-UI.s2 Rattus norvegicus cDNA, 3' end /clone=UI-R-C1-jz-h-03-0-UI /clone_end=3' /gb=AI045558 /ug=Rn.10801 /len=422
AI045858	13383	XM_027074	13384	XP_027074	13385			87n	ESTs, Weakly similar to T14794 hypothetical protein DKFZp586P 1522.1 [H.sapiens]		rc_AI045858 UI-R-C1-km-e-10-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-C1-km-e-10-0-UI /clone_end=3' /gb=AI045858 /ug=Rn.1740 /len=432
AI045858	13386	XM_027074	13387	XP_027074	13388			87n	ESTs, Weakly similar to T14794 hypothetical protein DKFZp586P 1522.1 [H.sapiens]		UI-R-C1-km-e-10-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-C1-km-e-10-0-UI /clone_end=3' /gb=AI045858 /ug=Rn.1740 /len=432

Table 3.

AI071511	13389	T41751		AB011399	13390	P55196	13391	91	Afadin		rc_AI071511 UI-R-C2-nc-h-01-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-C2-nc-h-01-0-UI /clone_end=3' /gb=AI071511 /ug=Rn.58 /len=427
AI072089	13392	JS0738		AB029042	13393	Q9UII2	13394	76	ATPase inhibitor (rat mitochondrial IF1 protein)		rc_AI072089 UI-R-C2-nf-d-09-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-C2-nf-d-09-0-UI /clone_end=3' /gb=AI072089 /ug=Rn.10960 /len=438
AI102917	13395	NP_112276	13396	D82348	13397	BAA11559	13398	91	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase (Atic)	NM_031014	rc_AI102917 EST212206 Rattus norvegicus cDNA, 3' end /clone=REMBU84 /clone_end=3' /gb=AI102917 /gi=3707555 /ug=Rn.11052 /len=458
AI104389	13399	AAK01620	13400	XM_032531		XP_032531		86n	Mus musculus ankyrin-repeat family A protein	AI104389	rc_AI104389 EST213678 Rattus norvegicus cDNA, 3' end /clone=RHECC67 /clone_end=3' /gb=AI104389 /gi=3708757 /ug=Rn.11082 /len=488
AI104389	13401	1TOH	13402	M20912	13403	I55282		88	Tyrosine hydroxylase		rc_AI104389 EST213678 Rattus norvegicus cDNA, 3' end /clone=RHECC67 /clone_end=3' /gb=AI104389 /gi=3708757 /ug=Rn.11082 /len=488
AI104882	13404	NP_075225	13405	XM_005114		XP_005114		71	Cytosolic epoxide hydrolase	NM_022936	rc_AI104882 EST214171 Rattus norvegicus cDNA, 3' end /clone=RHECK76 /clone_end=3' /gb=AI104882 /gi=3709128 /ug=Rn.11415 /len=401

Table 3.

AI105198	13406	NP_037162	13407	NM_003052	13408	NP_003043	13409	91	Solute carrier family 17 (sodium/hydrogen exchanger), member 2	NM_013030	EST214487 Rattus norvegicus cDNA, 3' end /clone=RKIBG82 /clone_end=3' /gb=AI105198 /ug=Rn.3542 /len=522
AI105374	13410	NP_036810	13411	NM_003290	13412	NP_003281	13413	60	Tropomycin 4	NM_012678	rc_AI105374 EST214663 Rattus norvegicus cDNA, 3' end /clone=RKIBJ48 /clone_end=3' /gb=AI105374 /gi=3709468 /ug=Rn.11115 /len=492
AI112391	13414	NP_036769	13415	NM_002827	13416	NP_002818	13417	81	Protein-tyrosine phosphatase	NM_012637	rc_AI112391 UI-R-Y0-mn-h-02-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-Y0-mn-h-02-0-UI /clone_end=3' /gb=AI112391 /ug=Rn.11317 /len=316
AI136540	13418	NP_035750	13419	NM_006757	13420	NP_006748	13421	64	troponin T3, skeletal, fast (Tnnt3)	NM_011620	rc_AI136540 UI-R-C2p-nq-h-04-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-C2p-nq-h-04-0-UI /clone_end=3' /gb=AI136540 /ug=Rn.22504 /len=474
AI145177	13422	NP_062010	13423	XM_017593	13424	XP_017593	13425	72	Rattus norvegicus Zinc-finger transcription factor NGFI-C	NM_019137	rc_AI145177 UI-R-BT0-pt-h-08-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-BT0-pt-h-08-0-UI /clone_end=3' /gb=AI145177 /ug=Rn.9703 /len=336
AI145494	13426	D30411		U40215	13427	JC4940	13428	94	Synapsin II		UI-R-BT0-qf-f-12-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-BT0-qf-f-12-0-UI /clone_end=3' /gb=AI145494 /ug=Rn.506 /len=486
AI145494	13429	D30411		U40215	13430	JC4940	13431	94	Synapsin II		UI-R-BT0-qf-f-12-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-BT0-qf-f-12-0-UI /clone_end=3' /gb=AI145494 /ug=Rn.506 /len=486
AI145680	13432	CAA60116	13433	XM_001306		XP_001306		80	monocarboxylate transporter	X86216	rc_AI145680 UI-R-BT0-qd-b-09-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-BT0-qd-b-09-0-UI /clone_end=3' /gb=AI145680 /ug=Rn.6085 /len=464

Table 3.

AI170685	13434	BAA88301	13435	NM_005880	13436	NP_005871	13437	86	mDj3	AB028853	rc_AI170685 EST216621 Rattus norvegicus cDNA, 3' end /clone=RMUAZ92 /clone_end=3' /gb=AI170685 /gi=3710725 /ug=Rn.3904 /len=648
AI175900	13438	P41156	13439	J04101	13440	TVHUET	13441	98	transcription factor ets-1		rc_AI175900 EST219472 Rattus norvegicus cDNA, 3' end /clone=ROVBG93 /clone_end=3' /gb=AI175900 /ug=Rn.7142 /len=458
AI175900	13442	P41156	13443	J04101	13444	TVHUET	13445	98	transcription factor ets-1		rc_AI175900 EST219472 Rattus norvegicus cDNA, 3' end /clone=ROVBG93 /clone_end=3' /gb=AI175900 /ug=Rn.7142 /len=458
AI178267	13446	XM_010735		XP_010735				93n	Homo sapiens membrane protein CH1		rc_AI178267 EST221933 Rattus norvegicus cDNA, 3' end /clone=RPLCO32 /clone_end=3' /gb=AI178267 /ug=Rn.8478 /len=545
AI178267	13447	XM_010735		XP_010735				93n	Homo sapiens membrane protein CH1		rc_AI178267 EST221933 Rattus norvegicus cDNA, 3' end /clone=RPLCO32 /clone_end=3' /gb=AI178267 /ug=Rn.8478 /len=545
AI178267	13448	XM_010735		XP_010735				93n	Homo sapiens membrane protein CH1		EST221933 Rattus norvegicus cDNA, 3' end /clone=RPLCO32 /clone_end=3' /gb=AI178267 /ug=Rn.8478 /len=545
AI178267	13449	XM_010735		XP_010735				93n	Homo sapiens membrane protein CH1		EST221933 Rattus norvegicus cDNA, 3' end /clone=RPLCO32 /clone_end=3' /gb=AI178267 /ug=Rn.8478 /len=545
NM_031643	13450	NP_113831	13451	NM_002755	13452	NP_002746	13453	90	Mitogen activated protein kinase kinase 2	AI178835	rc_AI178835 EST222517 Rattus norvegicus cDNA, 3' end /clone=RSPBQ02 /clone_end=3' /gb=AI178835 /ug=Rn.5850 /len=486
AI179610	13454	1DVEA		NM_002133	13455	1QQ8A		79	Heme oxygenase		EST223333 Rattus norvegicus cDNA, 3' end /clone=RSPCJ56 /clone_end=3' /gb=AI179610 /ug=Rn.3160 /len=604

Table 3.

AI228674	13458	NP_058797	13457	XM_016774	13458	XP_016774	13459	60	Rattus norvegicus Peptidylprolyl isomerase A (cyclophilin A)	NM_017101	rc_AI228674 EST225369 Rattus norvegicus cDNA, 3' end /clone=RBRCX94 /clone_end=3' /gb=AI228674 /ug=Rn.1463 /len=465
AI229031	13460	NP_037050	13461	XM_012898		XP_012898		72	calcium channel alpha 1A	NM_012918	rc_AI229031 EST225726 Rattus norvegicus cDNA, 3' end /clone=RBRDD18 /clone_end=3' /gb=AI229031 /ug=Rn.11281 /len=528
AI229237	13462	AAF80990	13463	NM_000913	13464	NP_000904	13465	77	orphanin FQ receptor gene (OFQR)	AF216218	rc_AI229237 EST225932 Rattus norvegicus cDNA, 3' end /clone=RBRDF79 /clone_end=3' /gb=AI229237 /ug=Rn.9762 /len=513
AI230256	13466	NP_037192	13467	XM_002273		XP_002273		97	Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	NM_013060	rc_AI230256 EST226951 Rattus norvegicus cDNA, 3' end /clone=REMCU23 /clone_end=3' /gb=AI230256 /ug=Rn.3272 /len=499
AI230256	13468	NP_037192	13469	XM_002273		XP_002273		97	Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	NM_013060	EST226951 Rattus norvegicus cDNA, 3' end /clone=REMCU23 /clone_end=3' /gb=AI230256 /ug=Rn.3272 /len=499
AI230260	13470	P13862	13471	X16312	13472	P13862	13473	100	Casein kinase II beta subunit		EST226955 Rattus norvegicus cDNA, 3' end /clone=REMCU27 /clone_end=3' /gb=AI230260 /ug=Rn.11095 /len=430

Table 3.

AI230614	13474	Q9QXL7	13475	AF153191	13476	Q9Y5B8	13477	87	ATPase Na+/K+ transporting beta 1 polypeptide		AF036761 Rattus norvegicus stearoyl-CoA desaturase 2 mRNA, partial cds
AI230614	13478	Q9QXL7	13479	AF153191	13480	Q9Y5B8	13481	87	ATPase Na+/K+ transporting beta 1 polypeptide		EST227309 Rattus norvegicus cDNA, 3' end /clone=REMCZ06 /clone_end=3' /gb=AI230614 /ug=Rn.8925 /len=373
AI231500	13482	BAA19517	13483	NM_002767	13484	NP_002758	13485	93	phosphoribosylpyrophosphate synthetase-associated protein	D84434	rc_AI231500 EST228188 Rattus norvegicus cDNA, 3' end /clone=REMDK87 /clone_end=3' /gb=AI231500 /ug=Rn.2681 /len=601
AI231519	13486	NP_061996	13487	AJ271734	13488	CAC07404	13489	54	Sialyltransferase 7	NM_019123	rc_AI231519 EST228207 Rattus norvegicus cDNA, 3' end /clone=REMDL26 /clone_end=3' /gb=AI231519 /ug=Rn.6602 /len=482
AI232256	13490	P04166	13491	AB009282	13492	O43169	13493	73	Cytochrome b5, outer mitochondrial membrane isoform		rc_AI232256 EST228944 Rattus norvegicus cDNA, 3' end /clone=RKIBZ24 /clone_end=3' /gb=AI232256 /ug=Rn.10249 /len=566
AI234060	13494	NP_058757	13495	NM_002317	13496	NP_002308	13497	72	Lysyl oxidase	NM_017061	rc_AI234060 EST230748 Rattus norvegicus cDNA, 3' end /clone=RLUCU63 /clone_end=3' /gb=AI234060 /ug=Rn.11372 /len=363
AI235506	13498	NP_114456	13499	NM_006788	13500	NP_006779	13501	71	RalA binding protein 1	NM_032067	rc_AI235506 EST232068 Rattus norvegicus cDNA, 3' end /clone=ROVCS71 /clone_end=3' /gb=AI235506 /ug=Rn.7107 /len=640
AI235890	13502	CAA34850	13503			Null		No Human	MHC class I RT1.C/E (transmembrane protein)	X16979	rc_AI235890 EST232452 Rattus norvegicus cDNA, 3' end /clone=ROVCY26 /clone_end=3' /gb=AI235890 /ug=Rn.14674 /len=387

Table 3.

AI236721	13504	B49023	13505	AF142498	13506	Q9UN99	13507	93	14-3-3 protein gamma-subtype	EST233283 Rattus norvegicus cDNA, 3' end /clone=ROVDJ72 /clone_end=3' /gb=AI236721 /ug=Rn.2503 /len=345
H31722	13508			Null					EST (not recognized)	rc_H31722 EST106068 Rattus norvegicus cDNA, 3' end /clone=RPCAW93 /clone_end=3' /gb=H31722 /gi=977139 /ug=Rn.14586 /len=341
H33301	13509			Null					EST (not recognized)	rc_H33301 EST109157 Rattus norvegicus cDNA, 3' end /clone=RPNAM37 /clone_end=3' /gb=H33301 /gi=978718 /ug=Rn.14636 /len=383
H33448	13510			Null					EST (not recognized)	rc_H33448 EST109458 Rattus norvegicus cDNA, 3' end /clone=RPNAR85 /clone_end=3' /gb=H33448 /gi=978865 /ug=Rn.14640 /len=430
H33486	13511	XM_043207		XP_043207				82n	Homo sapiens hypothetical protein FLJ10385	rc_H33486 EST109536 Rattus norvegicus cDNA, 3' end /clone=RPNAS60 /clone_end=3' /gb=H33486 /gi=978903 /ug=Rn.23316 /len=395
S39221	13512	AAB22435	13513	NM_021569	13514	NP_067544	13515	96	NMDA receptor	S39221 NMDA receptor {alternatively spliced} [rats, forebrain, mRNA, 1052 nt]
S39221	13516	AAB22435	13517	NM_021569	13518	NP_067544	13519	96	NMDA receptor	S39221 NMDA receptor {alternatively spliced} [rats, forebrain, mRNA, 1052 nt]
S43408	13520	AAB23030	13521	NM_005588	13522	NP_005579	13523	74	Endopeptidase-24.18 alpha subunit	S43408 endopeptidase-24.18 alpha subunit [rats, kidney, mRNA, 2928 nt]
S43408	13524	AAB23030	13525	NM_005588	13526	NP_005579	13527	74	Endopeptidase-24.18 alpha subunit	S43408 endopeptidase-24.18 alpha subunit [rats, kidney, mRNA, 2928 nt]

Table 3.

S46785	13528	P35859	13529	M86826	13530	P35858	13531	77	Rattus norvegicus insulin-like growth factor binding protein complex acid-labile subunit gene, complete cds		S46785 insulin-like growth factor binding protein complex acid-labile subunit [rats, liver, mRNA, 2190 nt]
S54212	13532	AAB25290	13533	NM_001842	13534	NP_001833	13535	85	Ciliary neurotrophic factor receptor alpha component		S54212 ciliary neurotrophic factor receptor alpha component [rats, brain, mRNA, 1332 nt]
S56481	13536	AAB25520	13537	M29932	13538	AAA35550	13539	70	Beta 3-adrenergic receptor {spliced version}		S56481 beta 3-adrenergic receptor {spliced version} [rats, colonic tissue, mRNA, 1968 nt]
S58745	13540	AAB20032	13541	NM_003216	13542	NP_003207	13543	79	Thyrotroph embryonic factor=leucine zipper transcription factor		S58745 thyrotroph embryonic factor=leucine zipper transcription factor [rats, pituitary, mRNA, 817 nt]
NM_022847	13544	NP_074038	13545	NM_000926	13546	NP_000917	13547	95	Progesterone receptor	S64044	S64044 progesterone receptor steroid-binding domain [rats, mRNA Partial, 548 nt]
S65091	13548	XM_002992		XP_002992				86	Cyclic AMP phosphoprotein, 19kD		S65091 cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
S65091	13549	XM_002992		XP_002992				86	Cyclic AMP phosphoprotein, 19kD		S65091 cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]

Table 3.

S68736	13550	AAB29713	13551	XM_052590	13552	XP_052590	13553	80	Myosin heavy chain	S68736 myosin heavy chain [rats, CCl4-cirrhotic liver fat-storing cell line, mRNA, 2924 nt]
S68736	13554	AAB29713	13555	XM_052590	13556	XP_052590	13557	80	Myosin heavy chain mRNA	myosin heavy chain [rats, CCl4-cirrhotic liver fat-storing cell line, mRNA, 2924 nt]
S68944	13558	AAC60673	13559	XM_052596		XP_052596		60	Na+/Cl(-)-dependent neurotransmitter transporter	S68944 Na+/Cl(-)-dependent neurotransmitter transporter [rats, brain, mRNA, 3762 nt]
S68944	13560	AAC60673	13561	XM_052596		XP_052596		60	Na+/Cl(-)-dependent neurotransmitter transporter	S68944 Na+/Cl(-)-dependent neurotransmitter transporter [rats, brain, mRNA, 3762 nt]
S69160	13562	AAB29945	13563	NM_003301	13564	NP_003292	13565	87	Thyrotropin-releasing hormone receptor (TRH-R)	S69160 thyrotropin-releasing hormone receptor [rats, pituitary gland, mRNA Partial, 1239 nt]
S69383	13566	AAB30132	13567	NM_001140	13568	NP_001131	13569	70	12-lipoxygenase	S69383 12-lipoxygenase [rats, pineal glands, mRNA, 2216 nt]
S73007	13570	AAB20688	13571	NM_000345	13572	NP_000336	13573	73	synuclein SYN1	S73007 synuclein SYN1 {alternatively spliced} [rats, mRNA, 695 nt]
S75280	13574	AAB33049	13575	XM_038637		XP_038637		92	pre-mtHSP70	S75280 pre-mtHSP70=70 kda heat shock protein precursor [rats, hepatoma cells H4, mRNA Partial, 2090 nt]
S75997	13576	AAB33384	13577	NM_016553	13578	NP_057637	13579	74	Nucleoporin p62 homolog	S75997 nucleoporin p62 homolog {inverted repeats} [rats, Sprague-Dawley, testis, mRNA Partial, 1134 nt]
S76799	13580	NP_036645	13581	XM_006027	13582	XP_006027	13583	93n	BDNF=brain-derived neurotrophic factor {alternatively spliced}	S76799 BDNF=brain-derived neurotrophic factor {alternatively spliced} [rats, brain, mRNA Partial, 421 nt]

Table 3.

S78215	13584	AAB34333	13585	NM_002708	13586	NP_002699	13587	100	Protein phosphatase 1 alpha		protein phosphatase 1 alpha [rats, striatum, mRNA, 1404 nt]
S79676	13588	AAB35431	13589	XM_040782		XP_040782		70	Interleukin 1beta converting enzyme		S79676 interleukin-1 beta-converting enzyme [rats, mRNA Partial, 458 nt]
S80127	13590	NP_058740	13591	NM_000315	13592	NP_000306	13593	71	Rattus norvegicus Parathyroid hormone (Pth)	NM_017044	S80127 PTH-(1-84)=hypothalamic parathyroid hormone [rats, Sprague-Dawley, mRNA Partial, 671 nt]
S82627	13594	AAC05016	13595			Null			Rattus sp. homeodomain (pem) mRNA, partial cds		S82627 Rattus sp. homeodomain (pem) mRNA, partial cds
S83436	13596	AAB50831	13597	NM_015917	13598	NP_057001	13599	69	rGSTK1-1=glutahione S-transferase subunit 13	AI105137	EST214426 Rattus norvegicus cDNA, 3' end /clone=RKIBG10 /clone_end=3' /gb=AI105137 /gi=3709294 /ug=Rn.3847 /len=622
U01344	13600	P50297	13601	U80835	13602	g2245376	13603	76	Rattus norvegicus clone A-2 arylamine N-acetyltransferase mRNA, complete cds		U01344 Rattus norvegicus clone A-2 arylamine N-acetyltransferase mRNA, complete cds /cds=(975,1847) /gb=U01344 /gi=786257 /ug=Rn.11112 /len=2533
U03763	13604	AAA82112	13605	NM_000929	13606	NP_000920	13607	68	phospholipase		U03763UTR#1 RRU03763 Rattus rattus phospholipase mRNA, complete cds
U03763	13608	AAA82112	13609	NM_000929	13610	NP_000920	13611	68	phospholipase		U03763UTR#1 RRU03763 Rattus rattus phospholipase mRNA, complete cds
U03763	13612	AAA82112	13613	NM_000929	13614	NP_000920	13615	68	phospholipase		U03763UTR#1 RRU03763 Rattus rattus phospholipase mRNA, complete cds

Table 3.

U05989	13616	AAA16492	13617	U63809	13618	AAC24947	13619	78	Par-4 induced by effectors of apoptosis	U05989 Rattus norvegicus clone par-4 induced by effectors of apoptosis mRNA, complete cds /cds=(66,1064) /gb=U05989 /gi=456281 /ug=Rn.9127 /len=2122
U07971	13620	AAA21250	13621	NM_001482	13622	NP_001473	13623	90	L-arginine:glycine amidinotransferase	U07971 Rattus norvegicus Sprague-Dawley L-arginine-glycine amidinotransferase mRNA, partial cds /cds=(48,1319) /gb=U07971 /gi=475452 /ug=Rn.1500 /len=2260
U08260	13624	I78557	13625	L76224	13626	Q14957	13627	57	Glutamate receptor, ionotropic, N-methyl D-aspartate 2D	U08260 Rattus norvegicus Sprague-Dawley N-methyl-D-aspartate receptor NMDAR2D subunit mRNA, complete cds /cds=(85,4056) /gb=U08260 /gi=475551 /ug=Rn.10063 /len=4957
U09361	13628	AAA56909	13629	XM_005348	13630	XP_005348	13631	56	Rattus norvegicus clone p17.1 tenascin mRNA, partial cds	U09361 RNU09361 Rattus norvegicus clone p17.1 tenascin mRNA, partial cds
U09631	13632	AAB60459	13633	XM_004641		XP_004641		87	VIP2 vasoactive intestinal peptide receptor	U09631 Rattus norvegicus VIP2 vasoactive intestinal peptide receptor mRNA, complete cds /cds=(115,1428) /gb=U09631 /gi=495195 /ug=Rn.10011 /len=3357
U10279	13634	A54892	13635	U62968	13636	AAB53839	13637	82	Sodium-dependent nucleoside transporter (rCNT1) mRNA, complete cds	U10279 Rattus norvegicus Sprague-Dawley sodium-dependent nucleoside transporter (rCNT1) mRNA, complete cds /cds=(156,2102) /gb=U10279 /gi=510272 /ug=Rn.10517 /len=2401

Table 3.

U11071	13638			Null					Polyadenylate-binding protein-related protein mRNA, 3' end		U11071 RNPABPR2 Rattus norvegicus Sprague-Dawley polyadenylate-binding protein-related protein mRNA, 3' end
U15764	13639	AAA89109	13640	M69180	13641	AAA61765	13642	99	nonmuscle myosin heavy chain-A		U15764 RRU15764 Rattus norvegicus nonmuscle myosin heavy chain-A mRNA, partial cds
U16245	13643	AAA66221	13644	NM_001651	13645	NP_001642	13646	77	Aquaporin-5		U16245 Rattus norvegicus aquaporin-5 (AQP5) mRNA, complete cds /cds=(109,906) /gb=U16245 /gi=664759 /ug=Rn.10066 /len=1426
U17565	13647	AAC18424	13648	NM_005915	13649	NP_005906	13650	91	Rattus norvegicus intestinal DNA replication protein mRNA, partial cds	AI639082	Rat mixed-tissue library Rattus norvegicus cDNA clone rx05005 3', mRNA sequence [Rattus norvegicus]
U18942	13651	AAA65039	13652	X98559	13653	CAA67169	13654	80	double-stranded RNA-specific adenosine deaminase		U18942 Rattus norvegicus double-stranded RNA-specific adenosine deaminase mRNA, complete cds /cds=(19,3546) /gb=U18942 /gi=755816 /ug=Rn.10056 /len=3608
U19516	13655	Q64350	13656	U23028	13657	Q13144	13658	88	Rattus norvegicus initiation factor eIF-2Be mRNA, complete cds		U19516 Rattus norvegicus initiation factor eIF-2Be mRNA, complete cds /cds=(34,2184) /gb=U19516 /gi=924598 /ug=Rn.10607 /len=2488

Table 3.

U19516	13659	Q64350	13660	U23028	13661	Q13144	13662	88	Rattus norvegicus initiation factor eIF-2Be mRNA, complete cds	Rattus norvegicus initiation factor eIF-2Be mRNA, complete cds /cds=(34,2184) /gb=U19516 /gi=924598 /ug=Rn.10607 /len=2488
U24489	13663	g1336153		M26856	13664	g180964		70	Tenascin X	U24489 Rattus norvegicus tenascin-X mRNA, partial cds /cds=(0,614) /gb=U24489 /gi=841425 /ug=Rn.10225 /len=793
U26397	13665	AAB01069	13666	NM_004027	13667	NP_004018	13668	93	inositol polyphosphate 4-phosphatase	U26397 Rattus norvegicus inositol polyphosphate 4-phosphatase mRNA, complete cds /cds=(286,3105) /gb=U26397 /gi=944912 /ug=Rn.11215 /len=5582
U27322	13669	AAC52235	13670	NM_000707	13671	NP_000698	13672	75	arginine-vasopressin V1b receptor	U27322 Rattus norvegicus arginine-vasopressin V1b receptor mRNA, complete cds /cds=(541,1806) /gb=U27322 /gi=945040 /ug=Rn.10096 /len=2559
U28927	13673	AAC52867	13674	U27699	13675	AAA87029	13676	79	Na+/Cl-betaine/GABA transporter	U28927 Rattus norvegicus liver Na+/Cl-betaine/GABA transporter mRNA, complete cds /cds=(304,2190) /gb=U28927 /gi=881597 /ug=Rn.11352 /len=2561
U30381	13677	Q62806	13678	AF039019	13679	Q9UQR1	13680	97	Zinc finger protein 148	U30381 Rattus norvegicus zinc finger binding protein mRNA, complete cds /cds=(387,2771) /gb=U30381 /gi=1373020 /ug=Rn.11383 /len=2772
U30813	13681			Null					Aspartyl-tRNA synthetase (Psl-DRS1) pseudogene	U30813cds RNU30813 Rattus norvegicus aspartyl-tRNA synthetase (Psl-DRS1) pseudogene, complete cds
U32498	13682	AAC52265	13683	NM_021807	13684	NP_068579	13685	94	rsec8	U32498 RNU32498 Rattus norvegicus rsec8 mRNA, partial cds

Table 3.

U33287	13686	P51868	13687	D55655	13688	O14958	13689	87	CALSEQUESTRIN, CARDIAC MUSCLE ISOFORM PRECURSOR		U33287 Rattus norvegicus calsequestrin mRNA, complete cds /cds=(133,1374) /gb=U33287 /gi=988306 /ug=Rn.10111 /len=1681
U35244	13690	AAC52985	13691	NM_022916	13692	NP_075067	13693	93	vacuolar protein sorting homolog r-vps33a		U35244 Rat vacuolar protein sorting homolog r-vps33a mRNA, complete cds /cds=(66,1859) /gb=U35244 /gi=1477467 /ug=Rn.1285 /len=3269
U35244	13694	AAC52985	13695	NM_022916	13696	NP_075067	13697	93	vacuolar protein sorting homolog r-vps33a		U35244 Rat vacuolar protein sorting homolog r-vps33a mRNA, complete cds /cds=(66,1859) /gb=U35244 /gi=1477467 /ug=Rn.1285 /len=3269
U35245	13698	AAC52986	13699	AF308803	13700	AAG34680	13701	96	Rat vacuolar protein sorting homolog r-vps33b mRNA		U35245 RNU35245 Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds
U35245	13702	AAC52986	13703	AF308803	13704	AAG34680	13705	96	Vacuolar protein sorting homolog r-vps33b	AI059963	rc_AI059963 UI-R-C1-la-d-01-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-C1-la-d-01-0-UI /clone_end=3' /gb=AI059963 /ug=Rn.10661 /len=534
U35345	13706	AAA79064	13707	NM_002577	13708	NP_002568	13709	91	serine/threonine kinase		U35345 Rattus norvegicus serine/threonine kinase (gamma-PAK) mRNA, complete cds /cds=(48,1622) /gb=U35345 /gi=1016004 /ug=Rn.10116 /len=1756
U36771	13710	AAB39470	13711	XM_034422	13712	XP_034422	13713	90	sn-glycerol 3-phosphate acyltransferase		U36771 RNU36771 Rattus norvegicus glycerol 3-phosphate acyltransferase mRNA, nuclear gene encoding mitochondrial protein, partial cds

Table 3.

U36773	13714	AAB39470	13715	XM_034422	13716	XP_034422	13717	90	sn-glycerol 3-phosphate acyltransferase		U36773 RNU36773 Rattus norvegicus glycerol-3-phosphate acyltransferase mRNA, nuclear gene encoding mitochondrial protein, partial cds
U36773	13718	AAB39470	13719	XM_034422	13720	XP_034422	13721	90	sn-glycerol 3-phosphate acyltransferase		U36773 RNU36773 Rattus norvegicus glycerol-3-phosphate acyltransferase mRNA, nuclear gene encoding mitochondrial protein, partial cds
U36786	13722	AAA92008	13723	NM_020833	13724	NP_065684	13725	27	Putative pheromone receptor VN7		U36786 Rattus norvegicus putative pheromone receptor VN7 mRNA, complete cds /cds=(29,850) /gb=U36786 /gi=1039471 /ug=Rn.10227 /len=1055
U38253	13726	AAC52788	13727	NM_020365	13728	NP_065098	13729	87	Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds	AI639441	Rat mixed-tissue library Rattus norvegicus cDNA clone rx05013 3', mRNA sequence [Rattus norvegicus]
U38253	13730	AAC52788	13731	NM_020365	13732	NP_065098	13733	87	Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma)		U38253 Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds /cds=(88,1446) /gb=U38253 /gi=1537014 /ug=Rn.10577 /len=1470

Table 3.

U38253	13734	AAC52788	13735	NM_020365	13736	NP_065098	13737	87	Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds	AI639441	Rat mixed-tissue library Rattus norvegicus cDNA clone rx05013 3', mRNA sequence [Rattus norvegicus]
U40628	13738	S70009	13739	AF043244	13740	AAC34993	13741	81	Unknown Glu Pro dipeptide repeat protein		Rattus norvegicus clone BB.1.4.1 unknown Glu-Pro dipeptide repeat protein mRNA, complete cds /cds=(675,1094) /gb=U40628 /gi=1184695 /ug=Rn.4088 /len=1876
U40819	13742	AAC52355	13743	AF100763	13744	AAD43027	13745	91	Rattus norvegicus 5'-AMP-activated protein kinase alpha-1 catalytic subunit		U40819 RNU40819 Rattus norvegicus 5'-AMP-activated protein kinase alpha-1 catalytic subunit mRNA, complete cds
U47110	13746	AAB19127	13747	AF035582	13748	AAB88198	13749	94	peripheral plasma membrane protein CASK		U47110 Rattus norvegicus peripheral plasma membrane protein CASK mRNA, complete cds /cds=(357,3086) /gb=U47110 /gi=1199823 /ug=Rn.10616 /len=3819
U48247	13750	AAC72251	13751	NM_005953	13752	NM_005953		85	protein kinase C-binding protein Enigma		U48247 RNU48247 Rattus norvegicus protein kinase C-binding protein Enigma mRNA, complete cds
U48247	13753	AAC72251	13754	NM_005953	13755	NM_005953		85	protein kinase C-binding protein Enigma		U48247 RNU48247 Rattus norvegicus protein kinase C-binding protein Enigma mRNA, complete cds

Table 3.

U48592	13756	AAB03502	13757	NM_002182	13758	NP_002173	13759	86	Interleukin-1 receptor accessory protein	U48592 Rattus norvegicus interleukin-1 receptor accessory protein (IL-1) mRNA, complete cds /cds=(102,1814) /gb=U48592 /gi=1403699 /ug=Rn.10511 /len=1862
U49935	13760	AAB40713	13761	M90814	13762	AAA51927	13763	96	cyclin D3.	U49935mRNA RNU49935 Rattus norvegicus cyclin D3 gene, partial cds
U49935	13764	AAB40713	13765	M90814	13766	AAA51927	13767	96	cyclin D3.	U49935mRNA RNU49935 Rattus norvegicus cyclin D3 gene, partial cds
U50717	13768	AAC52643	13769	XM_012060		XP_012060		88	Synaptic density protein PSD-93 mRNA, partial cds	U50717 RNU50717 Rattus norvegicus synaptic density protein PSD-93 mRNA, partial cds
U55938	13770	AAB50061	13771	XM_008782	13772	XP_008782	13773	91	GD3 alpha 2,8-sialyltransferase mRNA	U55938 Rattus norvegicus GD3 alpha 2,8 sialyltransferase mRNA complete cds /cds=(52,1194) /gb=U55938 /gi=1903380 /ug=Rn.10969 /len=1426
U57049	13774	AAB01988	13775			Null			Methylenetetrahydrofolate reductase mRNA, partial cds	U57049 Rattus norvegicus methylenetetrahydrofolate reductase mRNA, partial cds /cds=(0,485) /gb=U57049 /gi=1354771 /ug=Rn.10494 /len=1250
U62667	13776	P97574	13777	U25997	13778	P52823	13779	95	Stanniocalcin 1	U62667 Rattus norvegicus stanniocalcin (rSTC) mRNA, complete cds /cds=(109,852) /gb=U62667 /gi=1762530 /ug=Rn.10647 /len=1004
U65007	13780	PC4221	13781	M15326	13782	TVHUME	13783	88	Met proto-oncogene	U65007 Rattus norvegicus hepatocyte growth factor receptor mRNA, complete cds /cds=(0,4148) /gb=U65007 /gi=1679659 /ug=Rn.10617 /len=4189
U67140	13784	AAB48590	13785	XM_028634		XP_028634		73	PSD-95/SAP90-associated protein-4	U67140 Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds /cds=(204,3182) /gb=U67140 /gi=1864092 /ug=Rn.11279 /len=3348

Table 3.

U68172	13786	AAB08481	13787	NM_002457	13788	NP_002448	13789	79	mucin (MUC2)	U68172mRNA RNU68172 Rattus norvegicus mucin (MUC2) gene, partial cds
U70372	13790	AAC53031	13791			Null		No Human	PAM COOH-terminal interactor protein 2	U70372 Rattus norvegicus PAM COOH-terminal interactor protein 2 mRNA, complete cds /cds=(0,1180) /gb=U70372 /gi=1698778 /ug=Rn.10509 /len=1345
U70988	13792	AAC52981	13793	NM_001557	13794	NP_001548	13795	70	Chemokine (C-X-C) receptor 2	U70988cds RNU70988 Rattus norvegicus CXC chemokine receptor (CXCR2) gene, complete cds
U72741	13796	P97840	13797	AB006782	13798	O00182	13799	73	Lectin, galactose binding, soluble 9 (Galectin-9)	U72741 Rattus norvegicus 36 Kd beta-galactoside binding lectin mRNA, complete cds /cds=(5,1069) /gb=U72741 /gi=2351552 /ug=Rn.10706 /len=1070
U73174	13800	AAB18132	13801	XM_005119		1GRT	13802	84	Rattus norvegicus glutathione reductase mRNA, complete cds	U73174 RNU73174 Rattus norvegicus glutathione reductase mRNA, complete cds
U73174	13803	AAB18132	13804	XM_005119		1GRT	13805	84	Rattus norvegicus glutathione reductase mRNA, complete cds	U73174 RNU73174 Rattus norvegicus glutathione reductase mRNA, complete cds
U73174	13806	AAB18132	13807	XM_005119		1GRT	13808	84	Rattus norvegicus glutathione reductase mRNA, complete cds	RNU73174 Rattus norvegicus glutathione reductase mRNA, complete cds
U75398	13809	AAB38708	13810	NM_001964	13811	NP_001955	13812	66	Krox-24 mRNA, partial cds	U75398 RNKROX1 Rattus norvegicus Krox-24 mRNA, partial cds

Table 3.

U75400	13813	AAB38315	13814	NM_004766	13815	NP_004757	13816	50	Coatomer beta subunit mRNA		RNCOABS2 Rattus norvegicus coatomer beta subunit mRNA, partial cds and 3' untranslated sequence
U75923	13817	AAB81886	13818			Null		No Human	Isoleucyl tRNA synthetase mRNA, partial cds and 3' untranslated sequence		U75923UTR#1 SEG_RNTRNAIS3 Rattus norvegicus isoleucyl tRNA synthetase mRNA, partial cds and 3' untranslated sequence
U75928	13819	NP_036788	13820	NM_003118	13821	NP_003109	13822	83	Secreted acidic cystein rich glycoprotein (osteonectin)	NM_012656	U75928UTR#1 RNU75928 Rattus norvegicus SPARC mRNA, 3' untranslated region, partial seqeunce
U76635	13823	AAB71495	13824	NM_005223	13825	NP_005214	13826	71	Deoxyribonu clease I (DNaseI) ??	AI639157	Rat mixed-tissue library Rattus norvegicus cDNA clone rx00682 3', mRNA sequence [Rattus norvegicus]
U76635	13827	AAB71495	13828	NM_005223	13829	NP_005214	13830	71	Deoxyribonu clease I (DNaseI) ??	AI639157	Rat mixed-tissue library Rattus norvegicus cDNA clone rx00682 3', mRNA sequence [Rattus norvegicus]
U76997	13831	AAB19066	13832	NM_005575	13833	NP_005566	13834	83	Insulin-regulated membrane aminopeptid ase IRAP		U76997 Rattus norvegicus insulin-regulated membrane aminopeptidase IRAP mRNA, complete cds /cds=(71,3148) /gb=U76997 /gi=1674502 /ug=Rn.10614 /len=3197
U81492	13835	AAC17704	13836	NM_000588	13837	NP_000579	13838	29	Interleukin-3 beta		U81492 Rattus norvegicus interleukin-3 beta mRNA, complete cds /cds=(23,532) /gb=U81492 /gi=1763670 /ug=Rn.10652 /len=562
U82623	13839	AAB91537	13840	NM_006788	13841	NP_006779	13842	71	cytocentrin		U82623 Rattus norvegicus cytocentrin mRNA, complete cds /cds=(119,2200) /gb=U82623 /gi=2697021 /ug=Rn.7107 /len=3602
AF375463	13843	AAK56958	13844	NM_032298	13845	NP_115674	13846	49	Synaptotagm in 10 mRNA	U85513	U85513 RNU85513 Rattus norvegicus synaptotagmin X mRNA, partial cds

Table 3.

U86635	13847	A29036	13848	J05459	13849	3GTUD	13850	87	Glutathione S-transferase, mu 5		U86635 RNU86635 Rattus norvegicus glutathione s-transferase M5 mRNA, complete cds
U86635	13851	A29036	13852	J05459	13853	3GTUD	13854	87	Glutathione S-transferase, mu 5		U86635 RNU86635 Rattus norvegicus glutathione s-transferase M5 mRNA, complete cds
U86635	13855	A29036	13856	J05459	13857	3GTUD	13858	87	Glutathione S-transferase, mu 5		RNU86635 Rattus norvegicus glutathione s-transferase M5 mRNA, complete cds
U87627	13859	Q63344	13860	U81800	13861	O15427	13862	88	Monocarboxylate transporter		U87627 Rattus norvegicus putative monocarboxylate transporter (MCT3) mRNA, complete cds /cds=(89,1504) /gb=U87627 /gi=2463650 /ug=Rn.10826 /len=2118
U90121	13863	AAB49723	13864	NM_000361	13865	NP_000352	13866	59	thrombomdulin		U90121 Rattus norvegicus thrombomodulin mRNA, partial cds /cds=(0,1385) /gb=U90121 /gi=1890291 /ug=Rn.10716 /len=1665
U90215	13867	AAB49989	13868	NM_005668	13869	NP_005659	13870	97	polysialyltransferase		U90215 RNU90215 Rattus norvegicus polysialyltransferase mRNA, partial cds
U91679	13871	AAC12859	13872	NM_017521	13873	NP_059991	13874	70	ETS domain transcription factor Pet-1 mRNA		U91679 Rattus norvegicus ETS domain transcription factor Pet-1 mRNA, complete cds /cds=(111,1133) /gb=U91679 /gi=3033418 /ug=Rn.9775 /len=1722
U91847	13875	AAB51285	13876	XM_043351		XP_043351		94	p38 mitogen activated protein kinase	AA924542	rc_AA924542 UI-R-A1-dz-e-12-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-A1-dz-e-12-0-UI /clone_end=3' /gb=AA924542 /gi=3071678 /ug=Rn.3293 /len=487
U92289	13877	AAB71762	13878	U31099	13879	Q13258	13880	65	Prostaglandin D2 receptor		U92289 Rattus norvegicus prostaglandin D2 receptor mRNA, complete cds /cds=(60,1133) /gb=U92289 /gi=2459874 /ug=Rn.11409 /len=1315

Table 3.

U92803	13881	AAB61572	13882	NM_001296	13883	NP_001287	13884	58	CC-chemokine-binding receptor JAB61		U92803 Rattus norvegicus CCR10-related receptor (rCCR10rR) mRNA, complete cds /cds=(134,1282) /gb=U92803 /gi=2213806 /ug=Rn.10771 /len=1348
U92897	13885	AAB53321	13886	XM_052131		XP_052131		86	Kv4.3 (potassium voltage-gated channel)		U92897 RNU92897 Rattus norvegicus Kv4.3 mRNA, partial cds
U95052	13887	AAC53095	13888	U76111	13889	AAC51166	13890	98n	Mus musculus translation repressor NAT1 mRNA, complete cds	U76112	U95052UTR#1 RNU95052 Rattus norvegicus translation repressor NAT1 mRNA, partial 3'UTR
U95052	13891	AAC53095	13892	U76111	13893	AAC51166	13894	98n	Mus musculus translation repressor NAT1 mRNA, complete cds	U76112	U95052UTR#1 RNU95052 Rattus norvegicus translation repressor NAT1 mRNA, partial 3'UTR
U95920	13895	AAB54066	13896	L27841	13897	A54103	13898	83	Pericentriolar material 1		Rattus norvegicus pericentriolar material PCM-1 (PCM-1) mRNA, partial cds /cds=(0,1079) /gb=U95920 /gi=2078540 /ug=Rn.11026 /len=1135
X00975	13899	P04466	13900	M21812	13901	AAA91848	13902	99	Myosin, light polypeptide 2, alkali; ventricular, skeletal, slow		X00975 Rat MLC2 gene for muscle myosin light chain 2 /cds=(56,565) /gb=X00975 /gi=56726 /ug=Rn.6534 /len=648

Table 3.

X00975	13903	P04466	13904	M21812	13905	AAA91848	13906	99	Myosin, light polypeptide 2, alkali; ventricular, skeletal, slow	X00975 Rat MLC2 gene for muscle myosin light chain 2 /cds=(56,565) /gb=X00975 /gi=56726 /ug=Rn.6534 /len=648
X00975	13907	P04466	13908	M21812	13909	AAA91848	13910	99	Myosin, light polypeptide 2, alkali; ventricular, skeletal, slow	X00975 Rat MLC2 gene for muscle myosin light chain 2 /cds=(56,565) /gb=X00975 /gi=56726 /ug=Rn.6534 /len=648
X00975	13911	P04466	13912	M21812	13913	AAA91848	13914	99	Myosin, light polypeptide 2, alkali; ventricular, skeletal, slow	X00975 Rat MLC2 gene for muscle myosin light chain 2 /cds=(56,565) /gb=X00975 /gi=56726 /ug=Rn.6534 /len=648
X00975	13915	P04466	13916	M21812	13917	AAA91848	13918	99	Myosin, light polypeptide 2, alkali; ventricular, skeletal, slow	Rat MLC2 gene for muscle myosin light chain 2 /cds=(56,565) /gb=X00975 /gi=56726 /ug=Rn.6534 /len=648
X00975	13919	P04466	13920	M21812	13921	AAA91848	13922	99	Myosin, light polypeptide 2, alkali; ventricular, skeletal, slow	Rat MLC2 gene for muscle myosin light chain 2 /cds=(56,565) /gb=X00975 /gi=56726 /ug=Rn.6534 /len=648
X03369	13923	CAA27067	13924	XM_004389		XP_004389		90	beta-tubulin T beta15	X03369 Rat mRNA for beta-tubulin T beta15 /cds=(8,1345) /gb=X03369 /gi=57428 /ug=Rn.11235 /len=1592

Table 3.

X04310	13925	CAA27850	13926	NM_004931	13927	NP_004922	13928	40	37K chain of CD8 antigen	X04310 Rat thymocyte mRNA for 37K chain of CD8 antigen /cds=(39,665) /gb=X04310 /gi=55917 /ug=Rn.10330 /len=1261
X15734	13929	P13444	13930	D49357	13931	Q00266	13932	95	S-ADENOSYL METHIONINE SYNTHETASE ALPHA AND BETA FORMS	X15734 Rat mRNA for s-adenosylmethionine synthetase /cds=(72,1265) /gb=X15734 /gi=57183 /ug=Rn.10418 /len=1840
X16554	13933	KIRTR1	13934	Y00971	13935	KIHUR1	13936	100	Phosphoribosyl pyrophosphate synthetase 1	Rat PRPSI mRNA for phosphoribosylpyrophosphate synthetase subunit I (EC 2.7.6.1) /cds=(111,1067) /gb=X16554 /gi=56976 /ug=Rn.9761 /len=1981
X53588	13937	CAA37657	13938	M69051	13939	Q05810	13940	93	Rat mRNA for glucokinase, alternatively spliced GK2	X53588 Rat mRNA for glucokinase, alternatively spliced GK2 (EC 2.7.1.1) /cds=(91,1488) /gb=X53588 /gi=56239 /ug=Rn.10447 /len=2326
X54400	13941	CAA38266	13942	XM_052255		XP_052255		87	Hepatocyte growth factor (scatter factor)	Rat mRNA for hepatocyte growth factor /cds=(41,2227) /gb=X54400 /gi=56353 /ug=Rn.10468 /len=2431
X55660	13943	CAA39193	13944	NM_002569	13945	NP_002560	13946	85	pcRF104 mRNA for furin	X55660 Rat pcRF104 mRNA for furin /cds=(443,2824) /gb=X55660 /gi=56171 /ug=Rn.3220 /len=4259
X55660	13947	CAA39193	13948	NM_002569	13949	NP_002560	13950	85	furin prepeptide	X55660 Rat pcRF104 mRNA for furin /cds=(443,2824) /gb=X55660 /gi=56171 /ug=Rn.3220 /len=4259

Table 3.

X56747	13951	CAA40069	13952	NM_002299	13953	NP_002290	13954	76	Rat mRNA for fetal intestinal lactase-phlorizin hydrolase	X56747cds RRFILPHR Rat mRNA for fetal intestinal lactase-phlorizin hydrolase precursor, partial
X57523	13955	CAA40742	13956	L21205	13957	AAC12903	13958	65	R.norvegicus mtp1 mRNA	X57523 R.norvegicus mtp1 mRNA /cds=(0,2224) /gb=X57523 /gi=56716 /ug=Rn.10763 /len=2664
X57523	13959	CAA40742	13960	NM_000593	13961	NP_000584	13962	65	mtp1	X57523 R.norvegicus mtp1 mRNA /cds=(0,2224) /gb=X57523 /gi=56716 /ug=Rn.10763 /len=2664
X59249	13963	CAA41937	13964	L20463	13965	AAA16365	13966	70	Putative G-protein coupled receptor	X59249 Rat mRNA for putative G-protein coupled receptor /cds=(128,1090) /gb=X59249 /gi=56307 /ug=Rn.22612 /len=1594
X61296	13967			Null				80	L1 retroposon, ORF2 mRNA (partial)	X61296cds#2 RNL1RTO2C R.norvegicus L1 retroposon, ORF2 mRNA (partial)
X63995	13968	S30604	13969	L05568	13970	A47398	13971	90	Solute carrier family 6 (neurotransmitter transporter, serotonin), member 4 (5-hydroxytryptamine (serotonin) transporter)	X63995 R.norvegicus NTT mRNA /cds=(160,2052) /gb=X63995 /gi=56779 /ug=Rn.1663 /len=3180
X66842	13972	P30994	13973	X77307	13974	P41595	13975	81	5-hydroxytryptamine (serotonin) receptor 2B	X66842 R.norvegicus SRL mRNA for stomach fundus serotonin receptor /cds=(226,1665) /gb=X66842 /gi=57304 /ug=Rn.10425 /len=2003

Table 3.

X72914	13976	CAA51419	13977	XM_009336	13978	XP_009336	13979	79	cartilage oligomeric matrix protein		X72914 R.norvegicus mRNA for cartilage oligomeric matrix protein /cds=(6,2273) /gb=X72914 /gi=297438 /ug=Rn.10343 /len=2410
X76453	13980	S42794	13981	X92814	13982	P53816	13983	82	Hras-revertant gene 107		Rattus norvegicus (Sprague Dawley) H-rev107 mRNA /cds=(97,579) /gb=X76453 /gi=433962 /ug=Rn.11377 /len=966
X77209	13984	P55083	13985	AF134726	13986	g4529894		94	Hsp70-3 gene		X77209 R.norvegicus Hsp70-3 gene /cds=(13,1938) /gb=X77209 /gi=1814002 /ug=Rn.22532 /len=2546
X77209	13987	CAA54424	13988	XM_004187		XP_004187		88	heat shock protein 70	AA875620	rc_AA875620 UI-R-E0-cv-d-12-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-cv-d-12-0-UI /clone_end=3' /gb=AA875620 /gi=2980568 /ug=Rn.2978 /len=387
X82152	13989	CAA57648	13990	XM_001782	13991	XP_001782	13992	81	fibromodulin		X82152 R.norvegicus mRNA for fibromodulin /cds=(53,1183) /gb=X82152 /gi=602883 /ug=Rn.8778 /len=2943
X83399	13993	CAA58316	13994	NM_001968	13995	NP_001959	13996	99	eIF-4E		X83399 R.norvegicus mRNA eIF-4E /cds=(48,701) /gb=X83399 /gi=1240052 /ug=Rn.11275 /len=1647
X94185	13997	CAA63895	13998	XM_017018		XP_017018		83	dual specificity phosphatase , MKP-3		X94185cds RNMKP3 R.norvegicus mRNA for dual specificity phosphatase, MKP-3
X95850	13999			Null				No Human	R.norvegicus mRNA for novel gene expressed in circadian manner, clone SCN8		X95850mRNA RNSCN8 R.norvegicus mRNA for novel gene expressed in circadian manner, clone SCN8
X97374	14000	CAA66043	14001	NM_006228	14002	NP_006219	14003	66	Prepronocice ptin	X97375	X97374exon RNPPNEX2 R.norvegicus gene encoding prepronociceptin, exon 2

Table 3.

X97443	14004	CAA06212	14005	X97442	14006	P49755	14007	96	Integral membrane protein Tmp21-I (p23)		X97443 R.norvegicus mRNA for transmembrane protein Tmp21-I /cds=(0,611) /gb=X97443 /gi=1360135 /ug=Rn.22674 /len=706
X97443	14008	CAA06212	14009	X97442	14010	P49755	14011	96	Integral membrane protein Tmp21-I (p23)		Rattus norvegicus mRNA for transmembrane protein Tmp21-I /cds=(0,611) /gb=X97443 /gi=1360135 /ug=Rn.22674 /len=706
Y00404	14012	CAA68465	14013	NM_000454	14014	NP_000445	14015	83	Copper-zinc-containing superoxide dismutase		Y00404 Rat mRNA for copper-zinc-containing superoxide dismutase /cds=(93,557) /gb=Y00404 /gi=57274 /ug=Rn.6059 /len=650
Z15123	14016	AAA42105	14017	BC000171	14018	AAH00171	14019	93	S-adenosylmethionine decarboxylase 1	M64274	Z15123exon#5 RNAMDX48 R.norvegicus S-adenosylmethionine decarboxylase gene, exons 4-8
Z15123	14020	AAA42105	14021	BC000171	14022	AAH00171	14023	93	S-adenosylmethionine decarboxylase 1	M64274	Z15123exon#5 RNAMDX48 Rattus norvegicus S-adenosylmethionine decarboxylase gene, exons 4-8
Z17319	14024	CAA78967	14025	J05073	14026	P15259	14027	76	Phosphoglyceromutase		Z17319 R.norvegicus gene for phosphoglyceromutase /cds=(1181,1942) /gb=Z17319 /gi=297110 /ug=Rn.9738 /len=2126
Z22812	14028	CAA80465	14029	NM_004633	14030	NP_004624	14031	58	Interleukin-1 receptor type 2		Z22812 R.norvegicus interleukin-1 receptor type 2 /cds=(123,1373) /gb=Z22812 /gi=311407 /ug=Rn.10758 /len=1380
Z50144	14032	NP_058889	14033	NM_016228	14034	NP_057312	14035	69	Kynurenine aminotransferase II	NM_017193	Z50144 R.norvegicus mRNA for kynurenine/alpha-aminoadipate aminotransferase /cds=(112,1389) /gb=Z50144 /gi=1050751 /ug=Rn.11133 /len=1807

Table 3.

Z78279	14036	CAB01633	14037	S64596	14038	AAB27856	14039	84	Collagen alpha1 type I	U75405	U75405UTR#1 RNU75405 Rattus norvegicus alpha 1 type I collagen mRNA, 3' untranslated region, partial sequence
Z78279	14040	CAB01633	14041	S64596	14042	AAB27856	14043	84	Collagen alpha1	M27207	M27207mRNA RATCOL1A1 Rattus norvegicus (clone pL6-3-1) alpha-1 type I collagen mRNA, 3' UTR
Z78279	14044	CAB01633	14045	S64596	14046	AAB27856	14047	84	Collagen alpha1 type I		Z78279 R.norvegicus mRNA for collagen alpha1 type I /cds=(0,4361) /gb=Z78279 /gi=2894105 /ug=Rn.2953 /len=5721
AJ001529	14048	T34021	14049	U26424	14050	2204254A	14051	96	Serine/threonine kinase 3 (Ste20, yeast homolog) STK3		AJ001529cds RNMST2KIN Rattus norvegicus mRNA for MST2 kinase
AJ002556	14052	CAA05555	14053	AB058781	14054	BAB47507	14055	63	E-STOP protein		AJ002556 RNAJ2556 Rattus norvegicus mRNA for STOP protein
AJ132230	14056	CAA10610	14057	XM_007275	14058	XP_007275	14059	67	B1 bradykinin receptor		AJ132230 RNO132230 Rattus norvegicus mRNA for B1 bradykinin receptor
AJ132230	14060	CAA10610	14061	XM_007275	14062	XP_007275	14063	69	B1 bradykinin receptor		RNO132230 Rattus norvegicus mRNA for B1 bradykinin receptor
D10108	14064	P28576	14065	NM_002607	14066	NP_002598	14067	92	R.norvegicus mRNA for platelet-derived growth factor A chain (partial)	Z14120	Z14120cds RNPDGFACP R.norvegicus mRNA for platelet-derived growth factor A chain (partial)
D12524	14068	BAA02094	14069	NM_000222	14070	NP_000213	14071	79	c-kit receptor tyrosine kinase.		D12524 RATCKITPO Rat mRNA for c-kit receptor tyrosine kinase

Table 3.

D13213	14072	BAA02500	14073	NM_000836	14074	NP_000827	14075	77	N-methyl-D-aspartate receptor subunit		D13213 RATNMDARD1 Rat mRNA for N-methyl-D-aspartate receptor subunit (NMDAR2D-1)
D13912	14076	AAB59730	14077	M14096	14078	A29815	14079	77	Cytochrome P450, subfamily IIIA, polypeptide 3		RATP450 Rat mRNA for cytochrome P-450
D13962	14080	2107313A	14081	M20681	14082	P11169	14083	83	Solute carrier family 2 A3 (neuron glucose transporter)		D13962 RATGLUT3 Rat mRNA for neuron glucose transporter
D16817	14084	BAA04092	14085	NM_000843	14086	NP_000834	14087	66	Metabotropic glutamate receptor mGluR7		D16817 RATMGRM Rat mRNA for metabotropic glutamate receptor mGluR7
D90401	14088	BAA14397	14089	XM_012353		XP_012353		75	Dihydrolipoamide succinyltransferase		D90401 RATAKGE2 Rat mRNA for dihydrolipoamide succinyltransferase
D90401	14090	BAA14397	14091	XM_012353		XP_012353		75	Dihydrolipoamide succinyltransferase		RATAKGE2 Rat mRNA for dihydrolipoamide succinyltransferase
E01050	14092	NP_085914	14093	NM_000030	14094	NP_000021	14095	76	Rattus norvegicus Alanine-glyoxylate aminotransferase (Serine-pyruvate aminotransferase) (Agxt), mRNA	NM_030656	E01050cds cDNA encoding rat serine pirwvate aminotransferase

Table 3.

E01050	14096	NP_085914	14097	NM_000030	14098	NP_000021	14099	76	Rattus norvegicus Alanine-glyoxylate aminotransferase (Serine-pyruvate aminotransferase) (Agxt), mRNA	NM_030656	E01050cds cDNA encoding rat serine pirwvate aminotransferase
E13557	14100	NP_068518	14101	XM_029712		XP_029712		86	Cysteine-sulfinate decarboxylase (Csad)	NM_021750	E13557cds Rat mRNA for GADII
E13557	14102	NP_068518	14103	XM_029712		XP_029712		86	Cysteine-sulfinate decarboxylase (Csad)	NM_021750	E13557cds *Rat mRNA for GADII*
L07380	14104	NP_036982	14105	XM_030066		XP_030066		79	growth hormone-releasing factor receptor		L07380 RATGHRFRG Rattus rattus (clone pGR2) growth hormone-releasing factor receptor mRNA sequence
L07380	14106	NP_036982	14107	XM_030066		XP_030066		79	growth hormone-releasing factor receptor		L07380 RATGHRFRG Rattus rattus (clone pGR2) growth hormone-releasing factor receptor mRNA sequence
L11035	14108	AF327018	14109	AAK27360				81n	Rat T-cell receptor alpha chain mRNA for RT1L haplotype		L11035 RATTCAXAS Rat T-cell receptor alpha chain mRNA for RT1L haplotype

Table 3.

L14002	14110			Null					Polymeric immunoglobulin receptor AATTAA-containing 3'UTR mRNA sequence	L14002UTR#1 RATPIGRB Rattus norvegicus polymeric immunoglobulin receptor AATTAA-containing 3'UTR mRNA sequence
L15556	14111	Q9QW07	14112	L41349	14113	Q15147	14114	97	Phospholipase C , beta4	Rattus norvegicus phospholipase C (BETA4) mRNA /cds=UNKNOWN /gb=L15556 /gi=404071 /ug=Rn.6155 /len=5278
L16995	14115	XM_008168		XP_008168				82n	Add1	L16995 RATADD1A Rat add1 mRNA sequence
L26293	14116			Null				No Human	FSH-regulated protein mRNA	L26293 Rattus norvegicus (clone 180) FSH-regulated protein mRNA /cds=UNKNOWN /gb=L26293 /gi=425470 /ug=Rn.10415 /len=3678
M13100	14117			Null					Rat long interspersed repetitive DNA sequence LINE3 (L1Rn)	M13100cds#2 RATLIN3A Rat long interspersed repetitive DNA sequence LINE3 (L1Rn)
M13100	14118			Null					Rat long interspersed repetitive DNA sequence LINE3 (L1Rn)	M13100cds#3 RATLIN3A Rat long interspersed repetitive DNA sequence LINE3 (L1Rn)
M13100	14119			Null					Long interspersed repetitive DNA sequence LINE3	M13100cds#6 RATLIN3A Rat long interspersed repetitive DNA sequence LINE3 (L1Rn)

Table 3.

M61725	14120	B40439	14121	X56687	14122	S18193	14123	98	Rat transcription factor UBF1 mRNA	M61725 RATUBF2 Rat transcription factor UBF2 mRNA
M61725	14124	B40439	14125	X56687	14126	S18193	14127	98	Rat transcription factor UBF1 mRNA	RATUBF2 Rat transcription factor UBF2 mRNA
M92430	14128	AAA19949	14129	NM_013964	14130	NP_039258	14131	88n	Rat neu differentiation factor mRNA	M92430 Rat neu differentiation factor mRNA /cds=UNKNOWN /gb=M92430 /gi=205665 /ug=Rn.10311 /len=1867
M99567	14132	A45493		U26425	14133	I38994		92	Rattus norvegicus phospholipase C beta-3 mRNA, partial cds	M99567 RATPHOCBE Rat phospholipase C beta-3 mRNA
M99567	14134	A45493		U26425	14135	I38994		92	Rattus norvegicus phospholipase C beta-3 mRNA, partial cds	M99567 RATPHOCBE Rat phospholipase C beta-3 mRNA
M99567	14136	A45493		U26425	14137	I38994		92	Rattus norvegicus phospholipase C beta-3 mRNA, partial cds	RATPHOCBE Rat phospholipase C beta-3 mRNA
U30788	14138			Null					Rattus norvegicus Tclone4 mRNA	U30788 Rattus norvegicus Tclone4 mRNA /cds=UNKNOWN /gb=U30788 /gi=1216374 /ug=Rn.6477 /len=2026
X00923	14139	CAA25439		L00021	14140	AAB59424	14141	45	Immunoglobulin epsilon heavy chain	X00923cds RNIGE01 Rat gene for immunoglobulin epsilon heavy chain

Table 3.

X06150	14142	P13255	14143	X62250	14144	S42627	14145	92	Glycine methyltransferase		X06150cds RNGMTR Rat mRNA for glycine methyltransferase (EC 2.1.1.20)
X06801	14146	CAA29957	14147	NM_001613	14148	NP_001604	14149	100	Rat mRNA for vaskular alpha-actin		X06801cds RNACTAV Rat mRNA for vaskular alpha-actin
X06801	14150	CAA29957	14151	NM_001613	14152	NP_001604	14153	100	Rat mRNA for vaskular alpha-actin		X06801cds RNACTAV Rat mRNA for vaskular alpha-actin
X06801	14154	CAA29957	14155	NM_001613	14156	NP_001604	14157	100	vaskular alpha-actin		X06801cds RNACTAV Rat mRNA for vaskular alpha-actin
X06801	14158	CAA29957	14159	NM_001613	14160	NP_001604	14161	100	vaskular alpha-actin		X06801cds RNACTAV Rat mRNA for vaskular alpha-actin
X16623	14162	CAA34620	14163	XM_003704		XP_003704		80	Neuraxin		X16623cds RSNEU Rat mRNA for neuraxin
X17607	14164	CAA35609	14165	XM_004030	14166	XP_004030	14167	87	Rat beta-2 adrenergic receptor		X17607cds RSB2AR Rat beta-2 adrenergic receptor gene
X51615	14168	AAD50911	14169	XM_007169		XP_007169		86n	connexin protein Cx26	AF170284	X51615 RRCX26 R.rattus RNA for connexin protein Cx26
X53052	14170	CAA37219	14171	NM_012064	14172	NP_036196	14173	85	Rat mRNA for main intrinsic protein		X53052cds RRMIP Rat mRNA for main intrinsic protein
X53455	14174	CAA37535	14175	XM_030840	14176	XP_030840	14177	69	microtubule-associated protein 2		X53455cds RRMAP2 Rat mRNA for microtubule-associated protein 2
X56327	14178	CAA39766	14179	V00508	14180	P02100	14181	75	Epsilon 2 globin		X56327cds RNEP2GL Rattus norvegicus epsilon 2 globin gene
X56327	14182	CAA39766	14183	V00508	14184	P02100	14185	75	Epsilon 2 globin		X56327cds RNEP2GL Rattus norvegicus epsilon 2 globin gene
X57988	14186	CAA41054	14187	NM_000318	14188	NP_000309	14189	88	Peroxisome assembly factor-1	E03344	E03344cds cDNA sequence of peroxisome forming factor

Table 3.

X62325	14190			Null				No Human	TcRValphaT 48a2 mRNA for T cell receptor V-alpha J-alpha		X62325cds RRTRT48A2 R.rattus TcRValphaT48a2 mRNA for T cell receptor V-alpha J-alpha
X62325	14191			Null				No Human	TcRValphaT 48a2 mRNA for T cell receptor V-alpha J-alpha		X62325cds RRTRT48A2 R.rattus TcRValphaT48a2 mRNA for T cell receptor V-alpha J-alpha
X62325	14192			Null				No Human	R.rattus TcRValphaT 48a2 mRNA for T cell receptor V-alpha J-alpha		X62325cds RRTRT48A2 R.rattus TcRValphaT48a2 mRNA for T cell receptor V-alpha J-alpha
X62325	14193			Null				No Human	R.rattus TcRValphaT 48a2 mRNA for T cell receptor V-alpha J-alpha		X62325cds RRTRT48A2 R.rattus TcRValphaT48a2 mRNA for T cell receptor V-alpha J-alpha
X62660	14194	CAB46530	14195	NM_000847	14196	NP_000838	14197	56	Glutathione transferase subunit 8		X62660mRNA RRGTS8 R.rattus mRNA for glutathione transferase subunit 8
X62950	14198	AAA40872	14199	XM_003009		XP_003009		76	carboxypeptidase B.	M23953	X62950mRNA RNPBUS30 R.norvegicus mRNA (pBUS30) with repetitive elements
X63410	14200	CAA45007	14201	S43859	14202	AAB23169	14203	59	Hydroxysteroid sulfotransferase		X63410cds RRHYDSUL R.rattus mRNA for hydroxysteroid sulfotransferase

Table 3.

X63722	14204	JS0675	14205	X53051	14206	P19320	14207	76	Vascular cell adhesion molecule 1		X63722cds RNVCAM1R R.norvegicus mRNA for vascular cell adhesion molecule-1
X65083	14208	P80299	14209	L05779	14210	P34913	14211	78	Cytosolic epoxide hydrolase		X65083cds RNCEHR R.norvegicus mRNA for cytosolic epoxide hydrolase
X65083	14212	P80299	14213	L05779	14214	P34913	14215	78	Cytosolic epoxide hydrolase		X65083cds RNCEHR Rattus norvegicus mRNA for cytosolic epoxide hydrolase
X66022	14216	S26731		U43843	14217	Q92782	14218	87	Neuro-d4		X66022mRNA#1 RNND4P R.norvegicus mRNA for neuro-D4 protein
X66840	14219	CAA47316	14220	XM_032360		XP_032360		71	microtubule associated protein 1A		X66840cds RNMAP1AP R.norvegicus mRNA for microtubule associated protein 1A (partial)
X68041	14221	CAA48177	14222	NM_003102	14223	NP_003093	14224	64	superoxide dismutase		X68041cds RNSODIS R.norvegicus mRNA for epididymal secretory superoxide dismutase
X83094	14225	CAA58149	14226	NM_005526	14227	NP_005517	14228	83	Heat shock transcription factor 1	AI172097	rc_AI172097 EST218092 Rattus norvegicus cDNA, 3' end /clone=RMUBU88 /clone_end=3' /gb=AI172097 /gi=3712137 /ug=Rn.20418 /len=570
X90475	14229	Q63518	14230	NM_004533	14231	NP_004524	14232	80n	myosin-binding protein	AI639096	Rat mixed-tissue library Rattus norvegicus cDNA clone rx00904 3', mRNA sequence [Rattus norvegicus]
X91988	14233	CAA63043	14234	XM_012642	14235	XP_012642	14236	94	Stat5b protein		X91988 R.norvegicus mRNA for Stat5b protein /cds=UNKNOWN /gb=X91988 /gi=1143541 /ug=Rn.11355 /len=2615
Y08140	14237	CAA69334	14238	NM_004821	14239	NP_004812	14240	76	Rattus norvegicus mRNA for eHand protein		Y08140 RNHLH336 Rattus norvegicus mRNA for eHand protein
Y09365	14241	CAA70542	14242	XM_003736	14243	XP_003736	14244	88	G-protein coupled receptor kinase 6		Y09365cds RRGPCRK6 R.rattus mRNA for G-protein coupled receptor kinase 6

Table 3.

Y09453	14245	CAA70602	14246	NM_000727	14247	NP_000718	14248	91	Calcium channel gamma subunit		Y09453cds RNY09453 R.norvegicus mRNA for calcium channel gamma subunit
Y12178	14249	CAA72878	14250			Null		No Human	R.norvegicus mRNA for bilitranslocase		Y12178 RNBILITRA R.norvegicus mRNA for bilitranslocase
Y17295	14251	g2317735	14252	D14662	14253	P30041	14254	91	Rattus norvegicus mRNA for thiol-specific antioxidant protein (1-Cys peroxiredoxin		Y17295cds RNO17295 Rattus norvegicus mRNA for thiol-specific antioxidant protein (1-Cys peroxiredoxin)
Y17295	14255	CAA76732	14256	NM_004905	14257	NP_004896	14258	91	thiol-specific antioxidant protein	AA892041	rc_AA892041 EST195844 Rattus norvegicus cDNA, 3' end /clone=RKIAL12 /clone_end=3' /gb=AA892041 /gi=3018920 /ug=Rn.2680 /len=606
Z21935	14259	CAA79929	14260	XM_008806		XP_008806		94	Protein kinase rMNK2		Z21935cds RNPROKINA Rattus norvegicus protein kinase rMNK2
Z49748	14261			Null					m4 cholinergic muscarinic receptor		Z49748exon RNM4CMREC R.norvegicus gene for m4 cholinergic muscarinic receptor
AB012933	14262	O88813	14263	D10040	14264	JX0202	14265	62	Acyl-CoA synthetase 5		"Rattus norvegicus mRNA for acyl-CoA synthetase 5, complete cds"
AF009604	14266	O35180	14267	X99664	14268	Q99963	14269	86	SH3 domain protein 2 C1		"Rattus norvegicus SH3p13 mRNA, partial cds /cds=(0,875) /gb=AF009604 /gi=2293469 /ug=Rn.5909 /len=1216"

Table 3.

AF012347	14270	g2689829	14271	D83761	14272	g2251106	14273	95	Smad8	"Rattus norvegicus Smad8 mRNA, complete cds /cds=(152,1456) /gb=AF012347 /gi=2689628 /ug=Rn.10862 /len=1611"
AF016184	14274	g2367617	14275	U20760	14276	P41180	14277	33	Putative pheromone receptor (Go-VN7) [Human extracellular calcium-sensing receptor -low hom]	"Rattus norvegicus putative pheromone receptor (Go-VN7) mRNA, complete cds /cds=(24,2417) /gb=AF016184 /gi=2367616 /ug=Rn.10812 /len=3909"
AF029357	14278	g2570935	14279	AL022727	14280	g3757726		48	Olfactory receptor-like protein	"AF029357cds Rattus norvegicus olfactory receptor-like protein gene, complete cds"
AF038591	14281	g2760920	14282	X95762	14283	g2584787	14284	95	Cytoplasmic aminopeptidase P (APP)	"Rattus norvegicus cytoplasmic aminopeptidase P (APP) mRNA, complete cds /cds=(44,1915) /gb=AF038591 /gi=2760919 /ug=Rn.3473 /len=2381"
AF039212	14285	AAB94937	14286	AF297093	14287	AAG30417	14288	64	UDP-glucuronosyltransferase 1A7 (UGT1A7) gene	"AF039212mRNA Rattus norvegicus UDP-glucuronosyltransferase 1A7 (UGT1A7) gene, promoter and partial cds"
AF039218	14289	T14039	14290	AC002583	14291	O14578	14292	96	Postsynaptic density protein (citron)	"Rattus norvegicus postsynaptic density protein (citron) mRNA, complete cds /cds=(612,5468) /gb=AF039218 /gi=2745839 /ug=Rn.10876 /len=5952"
AF053990	14293	I59362		U20760	14294	A56715	14295	43	Vomeronasal neurons putative pheromone receptor V2R2B	"Rattus norvegicus tissue-type vomeronasal neurons putative pheromone receptor V2R2B mRNA, partial cds /cds=(0,692) /gb=AF053990 /gi=2996023 /ug=Rn.9651 /len=719"

Table 3.

NM_021593	14296	NP_067604	14297	NM_003679	14298	NP_003670	14299	79	Kynurenine 3-hydroxylase	AF056031	"Rattus norvegicus kynurenine 3-hydroxylase mRNA, complete cds"
AF072892	14300	S28764	14301	U16306	14302	P13611	14303	60	Proteoglycan PG-M V3 isoform		"Rattus norvegicus versican V3 isoform precursor, mRNA, complete cds"
NM_013149	14304	NP_037281	14305	NM_001621	14306	NP_001612	14307	67	Aryl hydrocarbon receptor	AF082126	"Rattus norvegicus aryl hydrocarbon receptor (AHR) mRNA, alternatively spliced longer insertion variant, complete cds"
D14988	14308	I52849	14309	X70222	14310	S28155	14311	63	Hydroxysteroid sulfotransferase		"RATHSS2 Rat mRNA for hydroxysteroid sulfotransferase subunit, complete cds"
D17349	14312	BAA04164		NM_000767	14313	NP_000758	14314	65	"Cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6 (see 257 on this sheet)"		"D17349cds RATCYP6 Rat cytochrome P450 2B15 gene, exon 9"
D84418	14315	P52925	14316	X62534	14317	2001363A	14318	98	"High mobility group protein 2 (23, 45, 52 on d.s.)"		"Rat mRNA for chromosomal protein HMG2, complete cds /cds=(74,706) /gb=D84418 /gi=1304192 /ug=Rn.2874 /len=1072"
D88586	14319	P70709	14320	X15161	14321	P12724	14322	55	Rat mRNA for eosinophil cationic protein		"Rat mRNA for eosinophil cationic protein, complete cds /cds=(63,530) /gb=D88586 /gi=1669582 /ug=Rn.10626 /len=711"
NM_031016	14323	NP_112278	14324	AF385588	14325	AAK68113	14326	86	Muscarinic receptor m2	J03025	"Rat muscarinic cholinergic receptor mRNA, complete cds /cds=(451,1851) /gb=J03025 /gi=203461 /ug=Rn.10752 /len=2483"

Table 3.

J03577	14327	P17267	14328	M63154	14329	P27352	14330	79	Gastric intrinsic factor	"Rat gastric intrinsic factor mRNA, complete cds /cds=(12,1277) /gb=J03577 /gi=204683 /ug=Rn.10954 /len=1466"
J03806	14331	A31317	14332	M34667	14333	P19174	14334	96	"Phospholipase C, gamma 1"	"Rat phospholipase C mRNA, complete cds /cds=(94,3966) /gb=J03806 /gi=206323 /ug=Rn.11243 /len=5106"
J05509	14335	P18125	14336	X56088	14337	JH0859	14338	82	Cytochrom P450 (cholesterol hydroxylase 7 alpha) (see 257 on this sheet)	"J05509CompleteSeq Rat cytochrome P450 cholesterol 7-alpha-hydroxylase (P450 VII) mRNA, complete cds /cds=UNKNOWN /gb=J05509 /gi=203204 /ug=Rn.10737 /len=3561"
K03041	14339	OWRT	14340	D00230	14341	P00480	14342	91	Ornithine carbamoyltransferase	K03041mRNA RATOTCB Rat (Sprague-Dawley) ornithine carbamoyltransferase mRNA
L02634	14343	AAA92110	14344	S42457	14345	AAB22778	14346	80	cGMP-gated rod photoreceptor channel related mRNA sequence	RATPHOTOA Rat cGMP-gated rod photoreceptor channel related mRNA sequence
L03294	14347	Q06000	14348	M15856	14349	LIHUL	14350	92	Lipoprotein lipase	"Rattus norvegicus lipoprotein lipase mRNA, complete cds /cds=(174,1598) /gb=L03294 /gi=205214 /ug=Rn.3834 /len=3617"
L07380	14351	NP_036982	14352	XM_030066		XP_030066		79	Growth hormone-releasing factor receptor (16 on d.s.)	RATGHRFRG Rattus rattus (clone pGR2) growth hormone-releasing factor receptor mRNA sequence
L13202	14353	AAA41319	14354	NM_012183	14355	NP_036315	14356	100	HNF-3/fork-head homolog-2 [Rattus norvegicus] Blink	"RATHFH2 Rattus norvegicus HNF-3/fork-head homolog-2 (HFH-2) mRNA, complete cds"

Table 3.

L14002	14357			Null					Polymeric immunoglobulin receptor AATTAA-containing 3'UTR mRNA sequence		L14002UTR#1 RATPIGRB Rattus norvegicus polymeric immunoglobulin receptor AATTAA-containing 3'UTR mRNA sequence
L14322	14358	P10687	14359	AB011153	14360	g3043686		91	Phospholipase C-beta1		"L14322exon RATPHOSPHO Rattus norvegicus phospholipase C-beta1 gene, complete exon"
L32601	14361	P51652	14362	D17793	14363	P42330	14364	71	20-alpha-hydroxysteroid dehydrogenase (20-alpha-HSD)		"RAT20AHYDE Rat 20 alpha-hydroxysteroid dehydrogenase mRNA, complete cds"
D86373	14365	BAA25372	14366	XM_031118		XP_031118		85	acyl-coenzyme A:cholesterol acyltransferase (ACACT)	L42293	"L42293mRNA MUSACACT Mus musculus acyl-coenzyme A:cholesterol acyltransferase (ACACT) mRNA, complete cds"
L43592	14367	g1161230	14368	AF152498	14369	g5457045	14370	73	Protocadherin-3 (pcdh3)		"Rattus norvegicus protocadherin-3 (pcdh3) mRNA, complete cds /cds=(137,2530) /gb=L43592 /gi=1161229 /ug=Rn.10166 /len=3017"
M18530	14371	g204785	14372	S65921	14373	g425520	14374	70	"Anti-acetylcholine receptor antibody gene, kappa-chain, VJC region"		"M18530cds RATIGKAI Rat (R.sordidus) germline kappa-chain C-region gene, 3' end"

Table 3.

M18853	14375	F27579		M15565	14376	g338766	14377	58	Rat T-cell receptor active alpha-chain C-region mRNA clone TRA29	"Rat T-cell receptor active alpha-chain C-region mRNA, partial cds, clone TRA29 /cds=(0,796) /gb=M18853 /gi=207163 /ug=Rn.9949 /len=1110"
M21622	14378	P12840	14379	X06948	14380	P12319	14381	48	"Fc fragment of Ige, high affinity I, receptor for, alpha polypeptide"	"Rat high-affinity IgE receptor (Fc-epsilon-R-I) mRNA, complete cds, clones R8-2b and R3-3 /cds=(176,853) /gb=M21622 /gi=204109 /ug=Rn.9677 /len=1179"
M21842	14382	S20791		X04714	14383	g28780	14384	64	Apolipoprotein B (apoB)	"Rat apolipoprotein B (apoB) mRNA, 3' end /cds=(0,212) /gb=M21842 /gi=202952 /ug=Rn.10711 /len=405"
M25157	14385	P07632	14386	K00065	14387	DSHUCZ	14388	83	"Superoxide dimutase 1, soluble"	"M25157mRNA RATSODCZL Rat Cu, Zn superoxide dismutase mRNA, complete cds"
M33201	14389	g206459	14390	K03475	14391	g190672	14392	71	"Surfactant-associated protein 1 (pulmonary surfactant protein, SP-A)"	"Rat pulmonary surfactant-associated glycoprotein A (SP-A) mRNA, complete cds /cds=(55,801) /gb=M33201 /gi=206460 /ug=Rn.11343 /len=1602"
M34134	14393	P18342	14394	M19713	14395	P09493	14396	94	Tropomyosin 1 (alpha)	"Rat brain alpha-tropomyosin (TMBr-2) mRNA, complete cds /cds=(136,891) /gb=M34134 /gi=207356 /ug=Rn.1033 /len=1004"
M34384	14397	P21263	14398	X65964	14399	P48681	14400	45	Nestin	"Rat nestin mRNA, complete cds /cds=(127,5544) /gb=M34384 /gi=205663 /ug=Rn.9701 /len=5946"
M35601	14401	P06399	14402	NM_021871	14403	1FZA	14404	59	Alpha-fibrinogen	"Rat alpha-fibrinogen mRNA, 3' end /cds=(0,281) /gb=M35601 /gi=204139 /ug=Rn.5500 /len=511"

Table 3.

M57682	14405	P27732	14406	M83566	14407	A38198	14408	95	"Calcium channel, voltage-dependent, L type, alpha 1D subunit"	"Rat brain calcium channel alpha-1 subunit mRNA, complete cds /cds=(526,5466) /gb=M57682 /gi=206573 /ug=Rn.9826 /len=6978"
M64791	14409	AAA42066	14410			g1911490		65	Salivary proline-rich protein (RP4) gene	"Rat salivary proline-rich protein (RP4) gene, complete cds /cds=(34,642) /gb=M64791 /gi=206715 /ug=Rn.9844 /len=881"
M64793	14411	AAA42064	14412			A37232		36	Rat salivary proline-rich protein (RP15)	"Rat salivary proline-rich protein (RP15) gene, complete cds /cds=(34,858) /gb=M64793 /gi=206711 /ug=Rn.9842 /len=1572"
M77479	14413	P26435	14414	L21893	14415	Q14973	14416	78	"Solute carrier family 10 (sodium/bile acid cotransporter family), member 1"	"Rattus norvegicus sodium/bile acid cotransporter mRNA, complete cds /cds=(121,1209) /gb=M77479 /gi=206853 /ug=Rn.9913 /len=1663"
M80570	14417	I59558	14418	M96670	14419	A48980	14420	93	"Solute carrier family 6 (neurotransmitter transporter, dopamine), member 3"	"Rat dopamine transporter mRNA, complete cds /cds=(62,1921) /gb=M80570 /gi=310097 /ug=Rn.10093 /len=3386"
M88111	14421	P28573	14422	S80071	14423	Q99884	14424	97	"Rattus norvegicus high affinity L-proline transporter mRNA, complete cds"	"Rattus norvegicus high affinity L-proline transporter mRNA, complete cds /cds=(84,2069) /gb=M88111 /gi=205234 /ug=Rn.9863 /len=2722"

Table 3.

M89906	14425	AAA40918	14426	NM_021050	14427	NP_066388	14428	86	Cystic fibrosis transmembrane conductance regulator		"RATCFTR Rattus norvegicus cystic fibrosis transmembrane conductance regulator (CFTR) gene, partial cds"
AF056034	14429	g4003519	14430	XM_039665	14431	XP_039665	14432	79	F-actin binding protein b-Nexilin		"EST188920 Rattus norvegicus cDNA, 3' end /clone=RHEAA88 /clone_end=3' /gb=AA799423 /gi=2862378 /ug=Rn.6183 /len=625"
AA799464	14433	AB026906	14434	BAA81889	14435			90	SDHD gene for small subunit of cytochrome b of succinate dehydrogenase		"EST188961 Rattus norvegicus cDNA, 3' end /clone=RHEAB35 /clone_end=3' /gb=AA799464 /gi=2862419 /ug=Rn.3792 /len=662"
NM_010757	14436	NP_034887	14437	AF055376	14438	AAC27037	14439	53	Short form transcription factor C-MAF (c-maf) (46 on d.s.)	AA799744	"EST189241 Rattus norvegicus cDNA, 3' end /clone=RHEAE74 /clone_end=3' /gb=AA799744 /gi=2862699 /ug=Rn.3818 /len=616"
AA799792	14440	P07882	14441	XM_005330		1717328A		78	Carboxyl ester lipase		"EST189289 Rattus norvegicus cDNA, 3' end /clone=RHEAF41 /clone_end=3' /gb=AA799792 /gi=2862747 /ug=Rn.7461 /len=615"
AA799883	14442			Null					EST(not recognised)		"EST189380 Rattus norvegicus cDNA, 3' end /clone=RHEAG50 /clone_end=3' /gb=AA799883 /gi=2862838 /ug=Rn.6252 /len=496"
AA800005	14443	Q9QZA6	14444	U14650	14445	P48509	14446	92	Platelet endothelial tetraspan antigen-3		"EST189502 Rattus norvegicus cDNA, 3' end /clone=RHEAI20 /clone_end=3' /gb=AA800005 /gi=2862960 /ug=Rn.1465 /len=828"
AA800210	14447			Null					EST(not recognised)		"EST189707 Rattus norvegicus cDNA, 3' end /clone=RHEAM47 /clone_end=3' /gb=AA800210 /gi=2863165 /ug=Rn.13244 /len=582"

Table 3.

									"ESTs, Weakly similar to AP17 CLATHRIN COAT ASSEMBLY PROTEIN AP17 [R.norvegicus]"		"EST189774 Rattus norvegicus cDNA, 3' end /clone=RHEAN32 /clone_end=3' /gb=AA800277 /gi=2863232 /ug=Rn.6307 /len=698"
AA800277	14448	Q00380	14449	X97074	14450	P53680	14451	43			
									Nuclear pore complex protein		"UI-R-A0-ah-h-10-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-A0-ah-h-10-0-UI /clone_end=3' /gb=AA818240 /gi=2888120 /ug=Rn.1347 /len=603"
AA818240	14452	P49791	14453	Z25535	14454	P49790	14455	82			
									EST(not recognised)		"UI-R-E0-bq-f-02-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-bq-f-02-0-UI /clone_end=3' /gb=AA858570 /gi=2948910 /ug=Rn.754 /len=520"
AA858570	14456			Null							
									EST(not recognised)		"UI-R-E0-cg-b-10-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-cg-b-10-0-UI /clone_end=3' /gb=AA859916 /gi=2949436 /ug=Rn.21405 /len=536"
AA859916	14457			Null							
									Rattus norvegicus mRNA for RP59 protein	AA859992	"UI-R-E0-ca-a-11-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-ca-a-11-0-UI /clone_end=3' /gb=AA859992 /gi=2949512 /ug=Rn.22633 /len=463"
AJ302650	14458	CAC16090	14459	XM_047360		XP_047360		38			
									EST(not recognised)		"UI-R-A0-bg-e-06-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-A0-bg-e-06-0-UI /clone_end=3' /gb=AA866221 /gi=2961667 /ug=Rn.3002 /len=146"
AA866221	14460			Null							
									EST(not recognised)		"UI-R-A0-ac-e-09-0-UI.s3 Rattus norvegicus cDNA, 3' end /clone=UI-R-A0-ac-e-09-0-UI /clone_end=3' /gb=AA866290 /gi=2961751 /ug=Rn.3045 /len=341"
AA866290	14461			Null							

Table 3.

AA866472	14462	2008109A		M86667	14463	S40510	14464	97	Nucleosome assembly protein 1-like 1		"UI-R-E0-br-g-09-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-br-g-09-0-UI /clone_end=3' /gb=AA866472 /gi=2961933 /ug=Rn.3121 /len=522"
AA874830	14465	KXRTS		L13720	14466	B48089	14467	75	"ESTs, Weakly similar to VITAMIN K-DEPENDENT PROTEIN S PRECURSOR [R.norvegicus]"		"UI-R-E0-cg-f-04-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-cg-f-04-0-UI /clone_end=3' /gb=AA874830 /gi=2979778 /ug=Rn.3138 /len=396"
AA874857	14468	AC004854	14469	Null				89	EST		"UI-R-E0-cg-h-12-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-cg-h-12-0-UI /clone_end=3' /gb=AA874857 /gi=2979805 /ug=Rn.3147 /len=454"
X56328	14470	CAA39767	14471	NM_005330	14472	NP_005321	14473	76	Epsilon 3 globin gene	AA875199	"UI-R-E0-cu-c-08-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-cu-c-08-0-UI /clone_end=3' /gb=AA875199 /gi=2980147 /ug=Rn.2827 /len=140"
AA875407	14474			Null					EST(not recognised)		"UI-R-E0-cs-a-11-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-E0-cs-a-11-0-UI /clone_end=3' /gb=AA875407 /gi=2980355 /ug=Rn.2908 /len=284"
AA891068	14475	g205986		S75037	14476	g802150		90	Peptidylglycine alpha-amidating monooxygenase		"EST194871 Rattus norvegicus cDNA, 3' end /clone=RHEAO60 /clone_end=3' /gb=AA891068 /gi=3017947 /ug=Rn.1121 /len=412"
AA891108	14477			Null					EST(not recognised)		"EST194911 Rattus norvegicus cDNA, 3' end /clone=RHEAP21 /clone_end=3' /gb=AA891108 /gi=3017987 /ug=Rn.22691 /len=513"

Table 3.

AA891834	14478			Null					EST(not recognised)		"EST195637 Rattus norvegicus cDNA, 3' end /clone=RKIAH39 /clone_end=3' /gb=AA891834 /gi=3018713 /ug=Rn.17094 /len=669"
AA891922	14479	AC021396	14480	Null				86	"Homo sapiens, clone RP11-281I2, complete sequence"		"EST195725 Rattus norvegicus cDNA, 3' end /clone=RKIAI64 /clone_end=3' /gb=AA891922 /gi=3018801 /ug=Rn.3690 /len=592"
AY027527	14481	AAK14799	14482	NM_016931	14483	NP_058627	14484	86	NADPH oxidase 4	AA892258	"EST196061 Rattus norvegicus cDNA, 3' end /clone=RKIAO28 /clone_end=3' /gb=AA892258 /gi=3019137 /ug=Rn.14744 /len=556"
AA892551	14485			Null					EST		"EST196354 Rattus norvegicus cDNA, 3' end /clone=RKIAS76 /clone_end=3' /gb=AA892551 /gi=3019430 /ug=Rn.14765 /len=112"
AA892762	14486			T12455				88	"ESTs, Moderately similar to T12455 hypothetical protein DKFZp564H2023.1 [H.sapiens]"		"EST196565 Rattus norvegicus cDNA, 3' end /clone=RKIAW93 /clone_end=3' /gb=AA892762 /gi=3019641 /ug=Rn.24893 /len=396"
AA892881	14487			Null					EST(not recognised)		"EST196684 Rattus norvegicus cDNA, 3' end /clone=RKIAY45 /clone_end=3' /gb=AA892881 /gi=3019760 /ug=Rn.14800 /len=545"
AA893043	14488			Null					EST(not recognised)		"EST196846 Rattus norvegicus cDNA, 3' end /clone=RKIBB45 /clone_end=3' /gb=AA893043 /gi=3019922 /ug=Rn.24959 /len=465"
AA893191	14489			Null					EST(not recognised)		"EST196994 Rattus norvegicus cDNA, 3' end /clone=RKIBD35 /clone_end=3' /gb=AA893191 /gi=3020070 /ug=Rn.3301 /len=654"

Table 3.

AA893314	14490			T12477				71	"ESTs, Moderately similar to T12477 hypothetical protein DKFZp564L0862.1 [H.sapiens]"	"EST197117 Rattus norvegicus cDNA, 3' end /clone=RKIBE92 /clone_end=3' /gb=AA893314 /gi=3020193 /ug=Rn.22749 /len=255"
AA893495	14491	P31211	14492	J02943	14493	A28321	14494	56	"ESTs, Highly similar to CORTICOSTEROID-BINDING GLOBULIN PRECURSOR [R.norvegicus]"	"EST197298 Rattus norvegicus cDNA, 3' end /clone=RLIAD19 /clone_end=3' /gb=AA893495 /gi=3020374 /ug=Rn.2374 /len=656"
AA893592	14495	Q62703	14496	D42073	14497	Q15293	14498	94	"ESTs, Weakly similar to RETICULOCALBIN 2 PRECURSOR [R.norvegicus]"	"EST197395 Rattus norvegicus cDNA, 3' end /clone=RPLAC34 /clone_end=3' /gb=AA893592 /gi=3020471 /ug=Rn.3275 /len=592"

Table 3.

									"ESTs, Weakly similar to HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 1 [R.norvegicus]"		"EST197474 Rattus norvegicus cDNA, 3' end /clone=RPLAI27 /clone_end=3' /gb=AA893671 /gi=3020550 /ug=Rn.22754 /len=399"
AA893671	14499	Q63244	14500	U02310	14501	1923399A	14502	93			
											"EST197628 Rattus norvegicus cDNA, 3' end /clone=RPLAM06 /clone_end=3' /gb=AA893825 /gi=3020704 /ug=Rn.8976 /len=402"
AA893825	14503			Null					EST(not recognised)		
									Peroxisomal integral membrane protein		"EST197893 Rattus norvegicus cDNA, 3' end /clone=RSPAQ64 /clone_end=3' /gb=AA894090 /gi=3020969 /ug=Rn.3737 /len=556"
AJ006341	14504	CAA06984	14505	NM_006358	14506	NP_006349	14507	83	PMP34	AA894090	
											"EST198140 Rattus norvegicus cDNA, 3' end /clone=RSPAW90 /clone_end=3' /gb=AA894337 /gi=3021216 /ug=Rn.7739 /len=397"
AA894337	14508			Null					EST (not recognised)		
											"UI-R-A1-eq-h-04-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-A1-eq-h-04-0-UI /clone_end=3' /gb=AA926149 /gi=3073285 /ug=Rn.3001 /len=449"
NM_012520	14509	NP_036652	14510	NM_001752	14511	NP_001743	14512	88	Catalase	AA926149	
									"Isocitrate dehydrogenase 1 (NADP+), soluble (IDH1)"		"EST199524 Rattus norvegicus cDNA, 3' end /clone=REMAA43 /clone_end=3' /gb=AA944025 /gi=3103941 /ug=Rn.3561 /len=537"
NM_031510	14513	NP_113698	14514	XM_028869	14515	XP_028869	14516	93		AA944025	
											"EST202041 Rattus norvegicus cDNA, 3' end /clone=RSPAZ69 /clone_end=3' /gb=AA946542 /gi=3106458 /ug=Rn.1928 /len=637"
NM_022537	14517	NP_071982	14518	X54393	14519	CAA38264	14520	30	Prolactin-like protein D	AA946542	

Table 3.

NM_024147	14521	NP_077061	14522	NM_016337	14523	NP_057421	14524	75	RNB6	AA997968	"UI-R-C0-hu-b-03-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-C0-hu-b-03-0-UI /clone_end=3' /gb=AA997968 /ug=Rn.9790 /len=529"
AI008741	14525	O35776	14526	U54804	14527	Q92819	14528	98	Hyaluronan synthase 2		"EST203192 Rattus norvegicus cDNA, 3' end /clone=REMBC59 /clone_end=3' /gb=AI008741 /ug=Rn.10781 /len=501"
NM_022713	14529	NP_073204	14530	NM_003241	14531	NP_003232	14532	52	Dorsal protein 1	AI013795	"EST208470 Rattus norvegicus cDNA, 3' end /clone=RSPBS90 /clone_end=3' /gb=AI013795 /ug=Rn.9984 /len=246"
AF057025	14533	P35859	14534	AF177765	14535	AAF05316	14536	62	Toll-like receptor 4	AI030997	"UI-R-C0-je-d-11-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-C0-je-d-11-0-UI /clone_end=3' /gb=AI030997 /ug=Rn.14534 /len=316"
AI044423	14537	P41276	14538	L28997	14539	P40616	14540	98	ADP-ribosylation factor-like 1		"UI-R-C1-jw-a-11-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-C1-jw-a-11-0-UI /clone_end=3' /gb=AI044423 /ug=Rn.11401 /len=387"
AI071511	14541	T41751		AB011399	14542	P55196	14543	91	Afadin (31 on d.s.)		"UI-R-C2-nc-h-01-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-C2-nc-h-01-0-UI /clone_end=3' /gb=AI071511 /ug=Rn.58 /len=427"
AI072435	14544	A23677	14545	J03827	14546	I39382	14547	97	Y box protein 1		"UI-R-C2-nk-c-03-0-UI.s1 Rattus norvegicus cDNA, 3' end /clone=UI-R-C2-nk-c-03-0-UI /clone_end=3' /gb=AI072435 /ug=Rn.3181 /len=488"
AI104389	14548	1TOH	14549	M20912	14550	I55282		88	Tyrosine hydroxylase		"EST213678 Rattus norvegicus cDNA, 3' end /clone=RHECC67 /clone_end=3' /gb=AI104389 /gi=3708757 /ug=Rn.11082 /len=488"
AI175900	14551	P41156	14552	J04101	14553	TVHUET	14554	98	transcription factor ets-1		"EST219472 Rattus norvegicus cDNA, 3' end /clone=ROVBG93 /clone_end=3' /gb=AI175900 /ug=Rn.7142 /len=458"
AI178012	14555	P33568	14556	NM_000321	14557	NP_000312	14558	90	Retinoblastoma 1 (including osteosarcoma)		"EST221669 Rattus norvegicus cDNA, 3' end /clone=RPLCJ92 /clone_end=3' /gb=AI178012 /ug=Rn.3485 /len=472"

Table 3.

AI232256	14559	P04166	14560	AB009282	14561	O43169	14562	73	"Cytochrome b5, outer mitochondrial membrane isoform"	"EST228944 Rattus norvegicus cDNA, 3' end /clone=RKIBZ24 /clone_end=3' /gb=AI232256 /ug=Rn.10249 /len=566"
AI638962	14563			Null					EST(not recognised)	"Rat mixed-tissue library Rattus norvegicus cDNA clone rx01189 3', mRNA sequence [Rattus norvegicus]"
AI638987	14564			Null					EST(not recognised)	"Rat mixed-tissue library Rattus norvegicus cDNA clone rx00568 3', mRNA sequence [Rattus norvegicus]"
AI638988	14565			Null					EST(not recognised)	"Rat mixed-tissue library Rattus norvegicus cDNA clone rx00508 3', mRNA sequence [Rattus norvegicus]"
AI639074	14566			Null					EST(not recognised)	"Rat mixed-tissue library Rattus norvegicus cDNA clone rx01925 3', mRNA sequence [Rattus norvegicus]"
AI639112	14567			Null					EST(not recognised)	"Rat mixed-tissue library Rattus norvegicus cDNA clone rx04824 3', mRNA sequence [Rattus norvegicus]"
AI639195	14568			Null					EST(not recognised)	"Rat mixed-tissue library Rattus norvegicus cDNA clone rx04881 3', mRNA sequence [Rattus norvegicus]"
AI639200	14569			Null					EST(not recognised)	"Rat mixed-tissue library Rattus norvegicus cDNA clone rx03240 3', mRNA sequence [Rattus norvegicus]"
AI639217	14570			Null					EST(not recognised)	"Rat mixed-tissue library Rattus norvegicus cDNA clone rx01420 3', mRNA sequence [Rattus norvegicus]"
AI639219	14571			Null					EST(not recognised)	"Rat mixed-tissue library Rattus norvegicus cDNA clone rx04760 3', mRNA sequence [Rattus norvegicus]"
AI639225	14572			Null					EST(not recognised)	"Rat mixed-tissue library Rattus norvegicus cDNA clone rx05060 3', mRNA sequence [Rattus norvegicus]"

Table 3.

AI639247	14573	AY009106	14574	AAG49397	14575			80	"EST, Moderately similar to T17296 hypothetical protein DKFZp434I092.1 [H.sapiens]"	"Rat mixed-tissue library Rattus norvegicus cDNA clone rx03939 3', mRNA sequence [Rattus norvegicus]"
AI639315	14576			Null					EST(not recognised)	"Rat mixed-tissue library Rattus norvegicus cDNA clone rx04457 3', mRNA sequence [Rattus norvegicus]"
AI639362	14577			Null					EST(not recognised)	"Rat mixed-tissue library Rattus norvegicus cDNA clone rx03215 3', mRNA sequence [Rattus norvegicus]"
AI639401	14578	L09190	14579	AAA65582	14580			81	Trichohyalin	"Rat mixed-tissue library Rattus norvegicus cDNA clone rx00654 3', mRNA sequence [Rattus norvegicus]"
AI639423	14581			Null					EST(not recognised)	"Rat mixed-tissue library Rattus norvegicus cDNA clone rx03133 3', mRNA sequence [Rattus norvegicus]"
AI639453	14582			Null					EST(not recognised)	"Rat mixed-tissue library Rattus norvegicus cDNA clone rx00152 3', mRNA sequence [Rattus norvegicus]"
NM_031669	14583	NP_113857	14584	No Human		Null			Uterine-specific proline-rich acidic protein	AI639531 "Rat mixed-tissue library Rattus norvegicus cDNA clone rx02618 3', mRNA sequence [Rattus norvegicus]"
NM_019349	14585	NP_062222	14586	AF273048	14587	AAG34908	14588	67	Serine/threonine kinase 2	H31623 "EST105855 Rattus norvegicus cDNA, 3' end /clone=RPCAT82 /clone_end=3' /gb=H31623 /gi=977040 /ug=Rn.14576 /len=404"
H31753	14589			Null					PC-12 cells (EST)	"EST106113 Rattus norvegicus cDNA, 3' end /clone=RPCAX41 /clone_end=3' /gb=H31753 /gi=977170 /ug=Rn.14591 /len=277"

Table 3.

H33448	14590			Null					EST(not recognised)	"EST109458 Rattus norvegicus cDNA, 3' end /clone=RPNAR85 /clone_end=3' /gb=H33448 /gi=978865 /ug=Rn.14640 /len=430"
H33750	14591	A42345	14592	AF151851	14593	AAD34088	14594	79	"ESTs, Weakly similar to D-BETA-HYDROXYBUTYRATE DEHYDROGENASE PRECURSOR [R.norvegicus]"	"EST110056 Rattus norvegicus cDNA, 3' end /clone=RPNAZ31 /clone_end=3' /gb=H33750 /gi=979167 /ug=Rn.8514 /len=468"
S46785	14595	P35859	14596	M86826	14597	P35858	14598	77	Insulin-like growth factor binding protein complex acid-labile subunit	"insulin-like growth factor binding protein complex acid-labile subunit [rats, liver, mRNA, 2190 nt]"
S58528	14599	AAB26277	14600	NM_002210	14601	NP_002201	14602	91	"Integrin, alpha V"	"integrin alpha v subunit [rats, NRK cells, mRNA Partial, 749 nt]"
S65091	14603	XM_002992		XP_002992				87	"Cyclic AMP phosphoprotein, 19kD"	"cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]"
S76489	14604	P52844	14605	U08098	14606	P49888	14607	71	Estrogen sulfotransferase	"estrogen sulfotransferase isoform 3 [rats, male, liver, mRNA, 1000 nt]"
S78744	14608	AAC60704	14609	Y00692	14610	AAA60181	14611	80	protein S=activated protein C cofactor	"protein S=activated protein C cofactor [rats, liver, mRNA, 3315 nt]"
S79676	14612	AAB35431	14613	XM_040782		XP_040782		70	Interleukin 1 beta converting enzyme	"interleukin-1 beta-converting enzyme [rats, mRNA Partial, 458 nt]"

Table 3.

S79711	14614	AAB21286	14615	NM_000073	14616	NP_000064	14617	64	CD3 gamma-chain		"CD3 gamma-chain [rats, mRNA, 620 nt]"
U07201	14618	P49088	14619	AC005326	14620	g3341715		93	Asparagine synthetase		"Rattus norvegicus asparagine synthetase mRNA, secondary transcript, complete cds /cds=(123,1808) /gb=U07201 /gi=460630 /ug=Rn.11172 /len=2226"
U07683	14621	A48801	14622	U30930	14623	Q16880	14624	93	UDP-glucuronosyltransferase 8		"Rattus norvegicus UDP-galactose-ceramide galactosyltransferase mRNA, complete cds /cds=(70,1695) /gb=U07683 /gi=464025 /ug=Rn.9744 /len=4185"
U08260	14625	I78557	14626	L76224	14627	Q14957	14628	57	"Glutamate receptor, ionotropic, N-methyl D-aspartate 2D"		"Rattus norvegicus Sprague-Dawley N-methyl-D-aspartate receptor NMDAR2D subunit mRNA, complete cds /cds=(85,4056) /gb=U08260 /gi=475551 /ug=Rn.10063 /len=4957"
NM_022854	14629	NP_074045	14630	X62167	14631	P02689	14632	59	Testis lipid binding protein	U09022	"Rattus norvegicus 15 kDa perforatorial protein PERF 15 mRNA, partial cds /cds=(33,431) /gb=U09022 /gi=538268 /ug=Rn.10078 /len=563"
U10096	14633	P55016	14634	U58130	14635	Q13621	14636	93	"Solute carrier family 12, member 1 (bumetanide-sensitive sodium-[potassium]-chloride cotransporter)"		"Rattus norvegicus Sprague-Dawley bumetanide-sensitive sodium-(potassium)-chloride cotransporter mRNA, complete cds /cds=(215,3502) /gb=U10096 /gi=507772 /ug=Rn.14799 /len=4595"
U10699	14637	JC1465	14638	M31210	14639	P21453	14640	50	G-protein coupled receptor 13		"Rattus norvegicus G-protein coupled receptor pH218 mRNA, complete cds /cds=(147,1205) /gb=U10699 /gi=505647 /ug=Rn.2491 /len=2754"
U30381	14641	Q62806	14642	AF039019	14643	Q9UQR1	14644	97	Zinc finger protein 148		"Rattus norvegicus zinc finger binding protein mRNA, complete cds /cds=(387,2771) /gb=U30381 /gi=1373020 /ug=Rn.11383 /len=2772"

Table 3.

U39206	14645	P51869	14646	AF054821	14647	g2997737	14648	78	P450 4F4 (CYP4F4) (see 257 on this sheet)	"Rattus norvegicus cytochrome P450 4F4 (CYP4F4) mRNA, complete cds /cds=(140,1708) /gb=U39206 /gi=1146435 /ug=Rn.10170 /len=2100"
U57062	14649	g1470062	14650	J03189	14651	g338011	14652	59	Natural killer cell protease 4 (RNKP-4) (47 on d.s.)	"Rattus norvegicus natural killer cell protease 4 (RNKP-4) mRNA, complete cds /cds=(9,755) /gb=U57062 /gi=1470061 /ug=Rn.10533 /len=868"
U67138	14653	g1864089	14654	AF009204	14655	g2454510		87	PSD-95/SAP90-associated protein-2	"Rattus norvegicus PSD-95/SAP90-associated protein-2 mRNA, complete cds /cds=(490,3432) /gb=U67138 /gi=1864088 /ug=Rn.10705 /len=3718"
U69278	14656	O08680	14657	M83941	14658	A38224	14659	95	Eph receptor A3	"Rattus norvegicus eph-related receptor tyrosine kinase homolog (Rek4) mRNA, complete cds /cds=(34,2988) /gb=U69278 /gi=1943913 /ug=Rn.10713 /len=3077"
U70825	14660	P97608	14661	AL096750	14662	g5419885		93	5-oxo-L-prolinase	"Rattus norvegicus 5-oxo-L-prolinase mRNA, complete cds /cds=(105,3971) /gb=U70825 /gi=1732064 /ug=Rn.3066 /len=4003"
U75358	14663	AAB53364	14664	XM_001880		XP_001880		85	myeloma protein kinase (PAK-2)	"RNU75358 Rattus norvegicus myeloma protein kinase (PAK-2) mRNA, partial cds"
U87627	14665	Q63344	14666	U81800	14667	O15427	14668	88	Monocarboxylate transporter	"Rattus norvegicus putative monocarboxylate transporter (MCT3) mRNA, complete cds /cds=(89,1504) /gb=U87627 /gi=2463650 /ug=Rn.10826 /len=2118"
U89744	14669	g1890275	14670	X63564	14671	P24928	14672	30	Rat putative cell surface antigen	"Rattus norvegicus putative cell surface antigen mRNA, complete cds /cds=(16,1659) /gb=U89744 /gi=1890274 /ug=Rn.10719 /len=2638"
U90215	14673	AAB49989	14674	NM_005668	14675	NP_005659	14676	97	Polysialyltransferase (51 on d.s.)	"RNU90215 Rattus norvegicus polysialyltransferase mRNA, partial cds"
X52082	14677	P17982	14678	S74683	14679	P52961	14680	42	RT6.2	X52082cds RNRT61 Rat mRNA for T-cell alloantigen RT6.1

Table 3.

X52952	14681	P00539	14682	J00119	14683	TVHUMS	14684	72	Moloney murine sarcoma viral (v-mos) oncogene homolog		"Rat mRNA for c-mos /cds=(846,1865) /gb=X52952 /gi=55965 /ug=Rn.10341 /len=3220"
X63446	14685	A32827	14686	M16961	14687	WOHU	14688	63	Alpha 2 HS-glycoprotein alpha 2 (fetuin)		"Rattus norvegicus mRNA for fetuin /cds=(31,1089) /gb=X63446 /gi=56139 /ug=Rn.3880 /len=1456"
X66842	14689	P30994	14690	X77307	14691	P41595	14692	81	5-hydroxytryptamine (serotonin) receptor 2B		"Rattus norvegicus SRL mRNA for stomach fundus serotonin receptor /cds=(226,1665) /gb=X66842 /gi=57304 /ug=Rn.10425 /len=2003"
X74549	14693	S41066	14694	X03498	14695	P05546	14696	85	Leuserpin-2		"Rattus norvegicus mRNA (rls2var1) for leuserpin-2 /cds=(119,1558) /gb=X74549 /gi=433612 /ug=Rn.10553 /len=2082"
X77209	14697	P55063	14698	AF134726	14699	g4529894		94	Hsp70-3 gene (7 on d.s.)		"Rattus norvegicus Hsp70-3 gene /cds=(13,1938) /gb=X77209 /gi=1814002 /ug=Rn.22532 /len=2546"
X89701	14700	CAA61848	14701	XM_036497	14702	XP_036497	14703	71	TPCR13 protein		X89701cds RNTPCR13P Rattus norvegicus mRNA for TPCR13 protein
NM_021741	14704	NP_068509	14705	AK022705	14706	BAB14190	14707	67	IP63 protein	X99330	X99330cds RNIAP27 Rattus norvegicus mRNA for IP63 protein
Y17295	14708	g2317735	14709	D14662	14710	P30041	14711	91	Rattus norvegicus mRNA for thiol-specific antioxidant protein (1-Cys peroxiredoxin		Y17295cds RNO17295 Rattus norvegicus mRNA for thiol-specific antioxidant protein (1-Cys peroxiredoxin)

Table 3.

NM_017193	14712	NP_058889	14713	NM_016228	14714	NP_057312	14715	69	Kynurenine aminotransferase II	Z50144	"Rattus norvegicus mRNA for kynurenine/alpha-aminoadipate aminotransferase /cds=(112,1388) /gb=Z50144 /gi=1050751 /ug=Rn.11133 /len=1807"

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

Rat Gene Accession No.	Rat Protein Access. No.	Human Protein Access. No.	Human Gene Access. No.	% homology	Identity	Former Identifier	Naïve Intensity	CFA Intensity	Affymetrix Ratio	Ratio CFA/Naïve
AA892799					Mus musculus 18 days embryo cDNA, RIKEN		6557.7	400707.1	53.8	61.1048
Z46882	CAA86981	NP_001377	NM_001386	96	TOAD-64		134.4	8061.4	37.8	59.9807
M73701	AAA42149	NP_003273	NM_003282	92	troponin I.		20	2184.1	19.9	109.205
D38222	g1054835	Q16849	L18983	86	Tyrosine phosphatase-like protein IA-2a		20	2179.1	14.6	108.955
X76593	CAA55329	AAB60403	U36310	89	Glycerol-3-phosphate dehydrate dehydrogenase	U83880	255.5	4116	12.9	16.1096
NM_022245	NP_071581	XP_048473	XM_048473	88	cytochrome b5 (Cyb5	AA817685	20	3065.3	11.9	153.265
X16623	CAA34620	XP_003704	XM_003704	80	Neuraxin		20	2161.1	10.9	108.055
X78848	CAA55405	NP_000838	NM_000847	75	glutathione S-transferase Yc1 subunit	S72505	905.7	4082.7	10.3	4.50778
M11794	AAA41640		No Human		metallothionein	AI176456	5.1	1769.5	9.9	346.961
D28968	BAA06091	NP_000951	NM_000960	74	prostacyclin receptor		20	1475.1	8.9	73.755
X63594	CAA45138	NP_065390	NM_020529	85	NF-KAPPA B INHIBITOR ALPHA		20	771.4	8.5	38.57
NM_012949	NP_037081	XP_008524	XM_008524	93	muscle specific enolase	AA851223	20	994.7	8.4	49.735
H31118					Mus musculus adult male lung cDNA, RIKEN		211.7	1729.9	8.2	8.17147
U70372	AAC53031		no human		PAM COOH-terminal interactor protein 2		733.9	1573.5	7.8	2.14403
L19931	AAA16532	NP_006740	NM_006749	81	amphotropic murine retrovirus receptor		20	1400.4	7.6	70.02
X53087	CAA37256	NP_000580	NM_000589	43	interleukin 4		20	1643.6	7.6	82.18
X95399					M31 protein, exon 9.	AI009141	20	1524	7.1	76.2
D32209	BAA06908	NP_006296	NM_006305	81	leucine-rich acidic nuclear protein		20	1198.8	6.6	59.94
X53565	CAA37637	AAC39542	AF027516	44	trans-Golgi network integral membrane protein TGN38		20	1176	6.1	58.8
L24897	AAA72046	XP_052590	XM_052590	86	myosin heavy chain		3814.4	22938.6	6	6.01368
X13905	CAA32105	NP_004152	NM_004161	91	rab1B protein		135.1	1101	5.9	8.14952
AB017912	BAA33453	NP_005892	NM_005901	89	Smad2 protein		20	788.7	5.8	39.435
J03179	AAA41083	NP_001343	NM_001352	68	D-binding protein		20	791.7	5.7	39.585
L15079	AAA02937	NP_061337	NM_018849	69	P-glycoprotein		20	1545.9	5.5	77.295
AA800908					EST(not recognised)		20	894.6	5.3	44.73

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

K00998	AAA41029	NP_000758	NM_000767	72	cytochrome p-450e		173.1	1361.1	5.3	7.86308
M16407	AAA40861	NP_000731	NM_000740	84	muscarinic acetylcholine receptor m3		173.9	1031.8	5.3	5.93329
U12514	AAA20669	XP_037643	XM_037643	97	MSX-2		20	1075.7	5.2	53.785
Y17326	CAB56823	NP_006684	NM_006693	98	CDK106	AA799867	8856.9	44931.5	5	5.07305
M11710	AAB59717	XP_040882	XM_040882	94	carbamyl phosphate synthetase		25.2	1091.9	5	43.3294
D29960	BAA06227	NP_001876	NM_001885	46	alphaB crystallin-related protein	AI103838	201.4	922.3	4.6	4.57944
D17310	BAA04132	BAA99542	AB045829	69	Steroid 3-alpha-dehydrogenase		407.1	1301.3	4.6	3.19651
D38062	BAA07258	AAB81536	U89507	67	UDP Glucuronosyltransferase		20	706.2	4.6	35.31
D14989	BAA03634	AAB23169	S43859	58	hydroxysteroid sulfotransferase	AI169695	70.1	761.9	4.5	10.8688
M57276	AAA41775	NP_000551	NM_000560	71	leukocyte antigen MRC-OX44		20	679.5	4.5	33.975
AI639181					EST(not recognised)		603.2	2647.6	4.4	4.38926
U38253	AAC52788	NP_065098	NM_020365	87	Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds	AI639441	731.2	4150.8	4.4	5.6767
AA891571					Mus musculus ES cells cDNA, RIKEN		20	805.5	4.3	40.275
AF005203	AAC15252	NP_004961	NM_004970	68	insulin-like growth factor binding protein complex acid-labile subunit	AA924289	283.9	1222.5	4.3	4.30609
D28498	BAA05857	NP_002010	NM_002019	77	Flt-1 tyrosine kinase receptor		208.6	897.6	4.3	4.30297
AA799469					EST(not recognised)		20	753.8	4.2	37.69
M15402	AAA41396	AAH05332	BC005332	68	immunoglobulin kappa-chain VJ precursor		20	786.9	4.2	39.345
AA799964					Mus musculus 18 days embryo cDNA, RIKEN		261.3	1062.2	4.1	4.06506
AA875010	XP_005342	XP_005342	XM_005342	89n	similar to GTPase Rab14 (Homo Sapiens)		195.3	955.3	4.1	4.89145
AF022774	AAB95448	NP_008918	NM_006987	75	rabphilin-3a related protein		20	844	4.1	42.2
M99223	AAA40991	NP_005164	NM_005173	72	calcium transporting ATPase		2466.7	10057.9	4.1	4.07747
AF091566	AAC64589	NP_036492	NM_012360	74	isolate HTF-SP1 olfactory receptor		47	989.2	4	21.0468
D12769	BAA02236	NP_001197	NM_001206	91	BTE binding protein		951.1	4002.4	4	4.20818
H33448					EST(not recognised)		166.7	757.6	4	4.54469
L19998	AAA41644	I57945	L19999	74	Minoxidil sulfotransferase		20	715.7	4	35.785
X74549	S41086	P05546	X03498	85	Leuserpin-2		142.9	966.2	4	6.76137
AA859524					EST(not recognised)		93.9	808.3	3.9	8.58679
AA893357					EST(not recognised)		181.6	763.4	3.9	4.20374
Y09945	CAA71076		no human		putative integral membrane transport protein		37.1	809.7	3.9	21.8248
AA875639					EST(not recognised)		199.4	756	3.8	3.79137

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

NM_012788	NP_036920	AAA50599	U13897		drosophila discs-large tumor suppressor homologue (synapse associated					
				89	protein)	AA891297	308.2	1185.1	3.8	3.84523
AA891859					EST (not recognized)		20	522.1	3.8	26.105
AA892338					Mus musculus adult male colon cDNA, RIKEN		3.1	548.9	3.8	177.065
J04792	AAA66286	NP_002530	NM_002539	91	Ornitine decarboxylase		878.3	1757.8	3.8	2.00137
M86758	AAA41128	NP_005411	NM_005420	73	estrogen sulfotransferase		152.1	774.2	3.8	5.09007
X59736	CAA42414	XP_011329	XM_011329	95	sarcomeric mitochondrial creatine kinase		145.1	639.7	3.8	4.40868
AA800156					Mus musculus 0 day neonate skin cDNA, RIKEN		20	643.3	3.7	32.165
X00975	P04466	AAA91848	M21812	99	Myosin, light polypeptide 2, alkali; ventricular, skeletal, slow		4186.9	18794.8	3.7	4.48895
X16554	KIRTR1	KIHUR1	Y00971	100	Phosphoribosyl pyrophosphate synthetase 1		1418.8	1640.1	3.7	1.15598
AA892565					Mus musculus adult male kidney cDNA, RIKEN		20	1367.1	3.6	68.355
AF007890	AAC23442	0801190A	NM_000365	49	Rattus norvegicus resection-induced TPI (rs11) mRNA		220.5	1123.7	3.6	5.09615
AF077354	Q63617	P34932	AB023420	95	Ischemia responsive 94 kDa protein (irp94)		680.5	2473.3	3.6	3.63453
AI639532		XP_029894	XM_029894	90n	troponin C2, fast		4199.6	17909.7	3.6	4.26462
L00382	AAA42289	NP_003280	NM_003289	68	beta-tropomyosin and fibroblast tropomyosin 1		194	706.3	3.6	3.64072
AI070967	I59334	P39687	X75090	88	Acid nuclear phosphoprotein 32 (leucine rich)		267.8	925.2	3.5	3.45482
D87839	BAA25570	XP_007904	XM_007904	90	beta-alanine oxoglutarate aminotransferase		219.1	763.8	3.5	3.48608
U62316	AAB04023	AAC13721	AF058056	72	Solute carrier family 16 (monocarboxylic acid transporters), member 7		337	922.6	3.5	2.73769
A01157	CAA00136	NP_004181	NM_004190	74	prelingual lipase		280.7	1021.4	3.4	3.63876
AF334104	AAK29403	XP_052300	XM_052300	89n	nucleolar protein GU2	AA799576	725.9	2484.9	3.4	3.4232
AA875527					Mus musculus, clone IMAGE:4222865		20	677.1	3.4	33.855
AA892284					EST(not recognised)		121.1	875.9	3.4	7.23287
S79304	AAB21298		no human		cytochrome oxidase subunit I	AA893485	20	556.1	3.4	27.805
U10097	AAA21252	XP_027753	XM_027753	87	thiazide-sensitive sodium-chloride cotransporter		20	1063.2	3.4	53.16

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

X59736	CAA42414	XP_011329	XM_011329	95	sarcomeric mitochondrial creatine kinase		451.9	1318.7	3.4	2.91812
AF050663					Activity and neurotransmitter-induced early gene 11 (ania-11)		448.7	1466.7	3.3	3.26878
L29281	S50216	A39650	M35663	62	Protein kinase, interferon-inducible double stranded RNA dependent		137.8	596.3	3.3	4.32729
X15734	P13444	Q00266	D49357	95	S-ADENOSYLMETHIONINE SYNTHETASE ALPHA AND BETA FORMS		169.5	744.1	3.3	3.92665
X55812	CAA39332	NP_001831	NM_001840	95	Cannabinoid receptor 1		35.2	683.2	3.3	19.4091
X96663	CAA65444	NP_003920	NM_003929	93	ras-related GTPase Rab29	AA858977	247.4	780.9	3.2	3.15643
AA893237					Mus musculus mRNA, complete cds, clone:2-72		1382.9	5432.9	3.2	3.92863
AA945583	O70351	Q99714	NM_004493	88	Hydroxyacyl-Coenzyme A dehydrogenase, type II		311.3	993.4	3.2	3.19113
AB001982	BAA21777	XP_003199	XM_003199	90	growth hormone secretagogue receptor type 1a		202	735.4	3.2	3.64059
AF000899	AAC82319	XP_037529	XM_037529	83n	p58/p45 mRNA, alternatively spliced form		497.6	1616.1	3.2	3.24779
AF048828	AAD02476	MMHUP3	L06132	93	Voltage-dependent anion channel 1		1207.1	3877.2	3.2	3.212
AI639143					EST(not recognised)		20	500.9	3.2	25.045
H31914	P13383	P19338	M60858	84	Nucleolin		194.3	620.8	3.2	3.19506
L00088	AAA98533	XP_030823	XM_030823	85	myosin light chain		3003.4	9703.4	3.2	3.23081
L23863		XP_012027	XM_012027	88n	Rat Skn1i mRNA		861.8	832.6	3.2	0.96612
M10140	AAA40935	XP_030967	XM_030967	89	skeletal muscle creatine kinase composite		11220.6	36189.2	3.2	3.22525
AA799637					Mus musculus adult male tongue cDNA, RIKEN		80.3	867.1	3.1	10.7983
AA894282					EST(not recognised)		352.5	1086.9	3.1	3.0834
AB018104	BAA35123	NP_002534	NM_002543	59	lectin-like oxidized low-density lipoprotein receptor		4.8	578.2	3.1	120.458
AI045858		XP_027074	XM_027074	87n	ESTs, Weakly similar to T14794 hypothetical protein DKFZp586P1522.1 [H.sapiens]		228	818.5	3.1	3.58991
AI639304					EST(not recognised)		549.1	3388.6	3.1	6.17119
AI639490		XP_031423	XM_031423	95n	Homo sapiens PHD zinc finger transcription factor (PF1)		144.9	554	3.1	3.82333
AF003598	AAB61241	XP_029723	XM_029723	88n	beta-integrin	S44606	33.7	553.5	3.1	16.4243
X02412	CAA26259	CAA27243	X03541	66	striated muscle alpha-tropomyosin		6631.9	20853.9	3.1	3.14448

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

AA859921					28S ribosomal RNA		15060	44589.8	3	2.96081
AF053988	AAC08415		no human		putative pheromone receptor V2R1-1		127.1	681.8	3	5.36428
NM_009861	NP_033991	NP_001782	NM_001791	100	cell division cycle 42 homolog	AI227887	281	852.8	3	3.03488
AI639324					Homo sapiens clone SP329 unknown mRNA		470.9	911.7	3	1.93608
D45920	BAA08351	NP_006217	NM_006226	88	130kDa-Ins(1,4,5)P3 binding protein		117.9	540.5	3	4.58439
M58495	AAA41989	NP_000894	NM_000903	82	R.norvegicus NAD(P)H: quinone reductase		34.3	566.1	3	16.5044
U50355	AAC99552	NP_066290	NM_021010	42	neutrophil defensin 4		811.3	2406	3	2.96561
AA799687					EST(not recognised)		166.7	623.8	2.9	3.74205
AA891634					EST (not recognized)		184.8	514.3	2.9	2.78301
X80130	CAA56429	NP_005150	NM_005159	100	alpha-actin cardiac	AI104567	375.3	1712.2	2.9	4.56222
M80601	AAA42067	XP_035702	XM_035702	83	zinc finger protein (RP8)	AI176462	321.4	923.7	2.9	2.87399
U80818	AAB39192	NP_008967	NM_007036	74	pineal specific PG25	AI233219	174.9	736.2	2.9	4.20926
D12524	BAA02094	NP_000213	NM_000222	79	c-kit receptor tyrosine kinase.		20	544.8	2.9	27.24
D13555	BAA02753	XP_043766	XM_043766	85	T cell receptor zeta chain		423.9	649	2.9	1.53102
D88250	BAA25797	XP_006641	XM_006641	76	ESTs, Weakly similar to JC6554 probable serine proteinase [R.norvegicus]	AA799803	648.5	2588.9	2.9	3.99214
E00444		P13284	J03909	72	ESTs, Moderately similar to GILT (GAMMA-INTERFERON-INDUCIBLE PROTEIN IP-30) [H.sapiens]		260.3	781.3	2.9	3.00154
J00692					SEQUENCE WITHDRAWN FROM DATABASES		8077	23423.9	2.9	2.90007
M21622	P12840	P12319	X06948	48	Fc fragment of IgE, high affinity I, receptor for, alpha polypeptide		344.1	745.1	2.9	2.16536
U83895	AAB41443	NP_004753	NM_004762	98	sec7A		108.9	719	2.9	6.60239
X52820	CAA37003	NP_000406	NM_000415	65	islet amyloid polypeptide		195.6	725.6	2.9	3.70981
X89963	CAA62002	NP_003239	NM_003248	83	thrombospondin-4		934.6	2705.8	2.9	2.89514
U62858	AAD41533	NP_002074	NM_002083	94	glutathione peroxidase	AA800587	784.3	2206.4	2.8	2.81321
AA891220					EST (not recognized)		20	684.8	2.8	34.24
AA892271					EST (mouse chromosome)		165.4	515.1	2.8	3.11427
AF032120	AAC69268	NP_005707	NM_005716	84	Regulator of G-protein signaling 19		753.8	831.5	2.8	1.10308
NM_019192	NP_062065	CAA77836	Z11793	62	selenoprotein P, plasma, 1	AI230247	1982.9	5498.6	2.8	2.77301
M27886	AAA58780	XP_013061	XM_013061	90	6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase		386.1	762.5	2.8	1.97488

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

M82826	AAA41691	XP_050121	XM_050121		Rattus leucopus neurofibromatosis protein type I (NF1, type III splice variant) mRNA, 3' end		148.3	646.1	2.8	4.35671
S80118	AAB47049	XP_008479	XM_008479	99	nude		726.7	2013.2	2.8	2.77033
U04740	AAA18422	NP_000943	NM_000952	72	platelet-activating factor receptor		347.1	966.3	2.8	2.78392
U46958	AAA92921	XP_030326	XM_030326	78	CD44I		161.3	1027.2	2.8	6.36826
X00975	P04466	AAA91848	M21812	74	Myosin, light polypeptide 2, alkali; ventricular, skeletal, slow		4708.3	13325.4	2.8	2.83019
X15467	CAA33494	NP_000804	NM_000813	99	GABA(A) receptor beta-2 preprotein		203	760.1	2.8	3.74433
NM_017158	NP_058854	NP_000760	NM_000769	94	cytochrome P450, 2c39 (Cyp2c39),	AA818198	412.8	819.4	2.7	1.98498
NM_017073	NP_058769	XP_046468	XM_046468	72	glutamine synthetase (glutamate-ammonia ligase)	AA852004	1666.4	4479.7	2.7	2.68825
NM_012520	NP_036652	NP_001743	NM_001752	92	Catalase	AA926149	114.6	768	2.7	6.68412
AA945054	1AQA	1803548A	XM_008817	88	Cytochrome b5		1396.8	3803	2.7	2.72265
AI070295	S68690	P24522	L24498	88	DNA-damage-inducible transcript 1		35.7	509.5	2.7	14.2717
H31665				92	Mus musculus adult male stomach cDNA, RIKEN		232.4	707.7	2.7	3.04518
L17318	B48013	P24928		36	Proline-rich proteoglycan (PRPG2)		236.9	688.2	2.7	2.90502
M82855	AAA41059	NP_000763	NM_000772	64	cytochrome P-450 IIC13		91.5	580.8	2.7	6.34754
U23056	S71107	P31997	X52378	51	Carcinoembryonic antigen-related cell adhesion molecule		267.8	727.6	2.7	2.71695
U82612	AAB40865	CAA26536	X02761	91	fibronectin		70.2	542.3	2.7	7.72507
AF038388	AAC27698	NP_004454	NM_004463	54	actin-filament binding protein Frabin		20	1046.5	2.6	52.325
AF074482	AAD03335	AAD45867	AF099033	98	GABA-B receptor 2 (GABA-BR2)		20	1947.7	2.6	97.385
M15202	AAA96446		no human		troponin T class proteins	AI136540	7250.8	18746.9	2.6	2.58549
AI639410					Mus musculus adult male lung cDNA, RIKEN		271.2	706.4	2.6	2.60472
D25233	BAA04958	NP_000312	NM_000321	89	retinoblastoma 1		252.4	694.4	2.6	2.75119
NM_020075	NP_064460	NP_001960	NM_001969	80	eukaryotic initiation factor 5 (eIF-5) (Eif5),	K01677	603.6	1124.2	2.6	1.86249
L09656	AAA42115	NP_003196	NM_003205	83	Rat salivary-specific cAMP response element-binding protein alpha		492.7	1281.7	2.6	2.60138
U09870	AAC52161	XP_008068	XM_008068	86	major vault protein		292	1623.6	2.6	5.56027
U68168	AAC53206	NP_003928	NM_003937	82	L-kynurenine hydrolase		56.1	549.5	2.6	9.79501
X59993	Q63679	g3882205	AB018285	91	Putative zinc finger protein		133	1015.7	2.6	7.63684
X78855	CAA55411	CAA66977	X98332	74	organic cation transporter		321.7	1328.8	2.6	4.13056
NM_011129	NP_035259	NP_004565	NM_004574	88	septin 4 (Sept4),	AA800004	504.2	1298.7	2.5	2.57576
AA892362					EST(not recognised)		594	1478.9	2.5	2.48973

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

AA893014					EST(not recognised)		389.6	959.9	2.5	2.46381
NM_019143	NP_062016	AAA52462	M10905	85	Fibronectin 1 (Fn1)	AA955600	692	1754.9	2.5	2.53598
AF035963	AAC53546	NP_036338	NM_012206	54	kidney injury molecule-1		273.2	683.6	2.5	2.5022
NM_031137	NP_112399	AAA63263	M55169	89	tripeptidylpeptidase II	AI069990	217.3	833.7	2.5	3.83663
X16957	CAA34831	NP_000090	NM_000099	72	cysteine proteinase inhibitor cystatin C	AI231292	47717.7	118296.9	2.5	2.4791
AI638984					EST(not recognised)		255	828.7	2.5	3.2498
NM_008891	NP_032917	AAG33941	AF195139	65	pinin (Pnn	AI639151	133	550.1	2.5	4.13609
AI639438					EST(not recognised)		36.4	771.9	2.5	21.206
AJ293948	CAC08185	AAG52886	AF333387	93	Kelch related protein 1 (krp1 gene)	AI639444	221.6	558.2	2.5	2.51895
D00569	Q64591	Q16698	L26050							
				81	Rattus norvegicus mRNA for 2,4-dienoyl CoA reductase precursor, complete cds		238.8	591	2.5	2.47487
D12978	BAA02355	NP_002688	NM_002697	83	octamer binding protein		20	768	2.5	38.4
D38101	BAA07282	CAA84341	Z34810	68	L-type voltage-dependent calcium channel alpha 1 subunit		246	665.9	2.5	2.70691
D84477	BAA20863	NP_001655	NM_001664	100	RhoA		1445.5	4100.7	2.5	2.83687
L18948	AAA18214	NP_002956	NM_002965	64	intracellular calcium-binding protein		1509.3	3820.6	2.5	2.53137
L19112	g310149	Q01742	X56191	90	Rat (clone R2(A3B)) heparin-binding fibroblast growth factor receptor 2 (extracellular domain) mRNA, partial cds		303	762.5	2.5	2.5165
M60753	AAA40881	XP_033799	XM_033799	81	catechol-O-methyltransferase		258.6	656.7	2.5	2.53944
M83210	AAC12783		no human		neonatal submandibular gland proacinar cell protein		250.5	709.7	2.5	2.83313
U50948	AAC52910	NP_006628	NM_006637	52	taste bud receptor protein TB 567.		465.2	886.8	2.5	1.90628
X06150	P13255	S42627	X62250	92	Glycine methyltransferase		280.1	1596.5	2.5	5.69975
X63744	CAA45276	NP_004163	NM_004172	87	glutamate/aspartate transporter		141.9	567.9	2.5	4.00211
Z56277	CAA91216	NP_001820	NM_001829	68	CLC-5 chloride channel protein		121	633.4	2.5	5.23471
AF166267	AAG15432	AAH08881	BC008881	50	kinesin	AA818427	134.7	834.5	2.4	6.19525
U44803	AAC52623	NP_057455	NM_016371	81	ovarian-specific protein	AA874944	338.5	808.1	2.4	2.3873
AA892228		NP_006251	NM_006260	86	Protein-kinase, interferon-inducible double stranded RNA dependent inhibitor		412.5	977.9	2.4	2.37067
AA963682	P97570	A55575	U13616	94	Rattus norvegicus 190 kDa ankyrin isoform mRNA, complete cds		20	513.2	2.4	25.66
AF034899	JC5836	Q15062	L35475	44	Olfactory receptor-like protein (SCR D-9)		666.8	1584.2	2.4	2.37582

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

AI102562	SMRT1	SMHU1E	M10943	86	Metallothionein-1 (mt-1)		1117	2695.1	2.4	2.4128
AI104389	1TOH	I55282	M20912	88	Tyrosine hydroxylase		388.7	661.8	2.4	1.7026
NM_017235	NP_058931	NP_057455	NM_016371	81	hydroxysteroid 17-beta dehydrogenase 7 (Hsd17b7),	AI236145	494.7	946.2	2.4	1.91267
AI639267					EST(not recognised)		349.4	1108.5	2.4	3.17258
AI639362					EST(not recognised)		470.9	1134.8	2.4	2.40985
D28512	BAA05870	NP_115674	NM_032298	71	Synaptotagmin III		3468.3	8233	2.4	2.37379
D38492	BAA07504	XP_038719	XM_038719	95	neural adhesion molecule F3		2281.2	2501.2	2.4	1.09644
S74265	AAB32559	XP_030840	XM_030840	78	HMW MAP2		191.5	567.2	2.4	2.96188
S75997	AAB33384	NP_057637	NM_016553	74	Nucleoporin p62 homolog		201.4	566.5	2.4	2.81281
U33314	AAC52268	NP_002569	NM_002578	95	serine/threonine kinase beta-PAK		126.1	816.8	2.4	6.4774
U65486	AAB19102	NP_002434	NM_002443	45	beta-microseminoprotein		211.8	591.8	2.4	2.79415
AA799636					EST(not recognised)		234.4	829.2	2.3	3.53754
AA800202					EST(not recognised)		254.1	587.8	2.3	2.31326
AA874803		NP_008352	NC_001807	89	ESTs, Moderately similar to 0806162L protein URF5 [M.musculus]		255.7	891.7	2.3	3.48729
AA892280					EST(not recognised)		305.2	704.1	2.3	2.30701
AA893733	S40148	A34269	J02764	80	ESTs, Weakly similar to S40148 integrin alpha-7A chain - rat [R.norvegicus]		3197.1	13625.9	2.3	4.26196
AA943677	g1763306	g2432000	AF020202	74	Munc13-3		111	754.3	2.3	6.7955
AI176191					EST(not recognised)		144.9	837	2.3	5.7764
AI231354	P49186	P45984	L31951	98	Stress activated protein kinase alpha II		521.6	1192.5	2.3	2.28623
AI639512					EST(not recognised)		165	580.5	2.3	3.51818
D28581	BAA05917	NP_000950	NM_000959	83	prostaglandin F2-alpha receptor		263.8	531.9	2.3	2.0163
L10073	AAA40616	NP_076917	NM_024012	69	5-hydroxytryptamine receptor		383.8	881.3	2.3	2.29625
M20724	AAA41953		no human		proline-rich protein		237.9	736.2	2.3	3.09458
M35965	AAA42089	NP_003226	NM_003235	85	thyroglobulin (rTg-2).		367.1	840.9	2.3	2.29066
M62891	AAA41710	NP_002249	NM_002258	44	3.2.3 antigen protein		374.1	866.7	2.3	2.31676
S83320	AAB50733	NP_068771	NM_021952	91	HuD=neurospecific RNA binding protein		1104.3	2500.6	2.3	2.26442
S85184	AAB21516	NP_001903	NM_001912	75	Cyclic Protein-2 (CP-2) mRNA, partial cds		722.4	2050.4	2.3	2.83832
U66471	AAC52951	NP_006559	NM_006568	84	Rattus norvegicus cell growth regulator rCGR19 mRNA, complete cds		233.1	733.8	2.3	3.14801
X71127	CAA50440	XP_010666	XM_010666	60	complement protein C1r [illegible] chain		1114.9	2529.4	2.3	2.26872

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

Z22867	CAA80489	NP_000913	NM_000922	68	3',5'-cyclic AMP phosphodiesterase		201.4	624.8	2.3	3.10228
AA859911	Q11205	JC5251	U63090	93	Sialyltransferase 5		433.5	940.8	2.2	2.17024
AA875348					EST(not recognised)		501.5	1085.5	2.2	2.16451
AA891725					Mus musculus 13 days embryo head cDNA, RIKEN		415.4	904.4	2.2	2.17718
AA893160					EST(not recognised)		458.2	1027.3	2.2	2.24203
AA894340					EST(not recognised)		299.1	654	2.2	2.18656
U61261	AAB17053	XP_008772	XM_008772	77	laminin-5 alpha 3 chain	AA946108	235.6	516	2.2	2.19015
D21132	BAA04669	NP_036531	NM_012399	98	phosphatidylinositol transfer protein	AA998446	248.3	533.6	2.2	2.16646
AB010428	BAA32434	XP_040337	XM_040337	70	acyl-CoA hydrolase		544.3	1812	2.2	3.32905
AF078779	AAC68885	CAC40696	AL138707	89	Rattus norvegicus putative four repeat ion channel mRNA, complete cds		409	886.3	2.2	2.16699
M23572	AAB08828	NP_061821	NM_018948	74	gene 33	AI169756	819.3	2427.6	2.2	2.96302
J03753	AAA73898	NP_001673	NM_001682	91	plasma membrane Ca2+ ATPase	AI172499	217.4	505.2	2.2	2.32383
AI231445	P18395	BAA74908	AB020692	98	Rat unr mRNA for unr protein with unknown function		579.2	1297.3	2.2	2.23981
NM_023957	NP_076447	NP_056000	NM_015185	98	colibistin I	AI639196	482.4	1076	2.2	2.23051
AI639305					Mus musculus adult male testis cDNA, RIKEN		610.8	1956.8	2.2	3.20367
D00913	BAA00759	NP_000192	NM_000201	50	Intercellular adhesion molecule-1		20	1434.4	2.2	71.72
D14015	BAA03116	P24864	M73812	76	Cyclin E		20	2201.9	2.2	110.095
D63673	BAA09824	NP_000278	NM_000287	75	peroxisome assembly factor-2		736.5	1822.5	2.2	2.47454
L39991	AAC42054	BAB18537	AB040538	78	nucleoporin		361.7	787.4	2.2	2.17694
S81353	AAB36042	NP_002769	NM_002778	64	sulfated glycoprotein-1; SGP-1; prosaposin		22254	48442.1	2.2	2.17678
U19516	Q64350	Q13144	U23028	88	Rattus norvegicus initiation factor eIF-2Be mRNA, complete cds		20	533.3	2.2	26.665
U30186	AAA73629	XP_048609	XM_048609	65	GADD153		465.6	1013.3	2.2	2.17633
U51584	AAB17131	NP_110378	NM_030751	81	zinc finger homeodomain enhancer-binding protein-2		20	529.8	2.2	26.49
U92072	AAD04756	XP_045911	XM_045911	67	Tomosyn		509	1102	2.2	2.16503
X05472					Genomic 2.4 kb repeat DNA right terminal containing two ORFs		1069.5	2321.5	2.2	2.17064
X59859	CAA42519	NP_001911	NM_001920	74	decorin	AI639233	390.6	874	2.2	2.23758
X66022	S26731	Q92782	U43843	87	Neuro-d4		334.3	742.8	2.2	2.22196
NM_009266	NP_033292	NP_036380	NM_012248	78	selenophosphate synthetase 2	AA799700	371.5	768.5	2.1	2.06864

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

AA891438					Mus musculus adult male testis cDNA, RIKEN		535.1	1123.1	2.1	2.09886
AA892240					EST(not recognised)		2041.2	1316.8	2.1	0.64511
NM_031137	NP_112399	AAA63263	M55169	89	tripeptidyl peptidase II	AI071507	280	592.8	2.1	2.11714
NM_012678	NP_036810	NP_003281	NM_003290	60	Tropomycin 4 (Tpm4),	AI105374	144.9	1098.4	2.1	7.5804
D49708	BAA08556	AAD19278	AF057159	75	RNA binding protein (transformer-2-like)	AI231164	899	1854.3	2.1	2.08263
AF016049	AAC27975	NP_000421	NM_000430	99	platelet-activating factor acetylhydrolase beta subunit	AI234730	286.4	697.3	2.1	2.43471
AI638973					EST(not recognised)		48.4	728	2.1	15.0413
AI639136					EST(not recognised)		238.2	541	2.1	2.2712
AI639142					EST(not recognised)		335.1	687.6	2.1	2.05192
AI639195					EST(not recognised)		475.7	984.7	2.1	2.07
AF148797	AAD31539	AAA93514	L36531	77	alpha 8 integrin	AI639291	338.9	1182.5	2.1	3.48923
D10770	BAA01601	NP_002722	NM_002731	96	Rat mRNA for beta isoform of catalytic subunit of cAMP-dependent protein kinase		240.5	532.8	2.1	2.21538
D79215	BAA11468	NP_004456	NM_004465	86	FGF-10		281	580.1	2.1	2.06441
D86373	BAA25372	XP_031118	XM_031118	85	acyl-coenzyme A:cholesterol acyltransferase (ACACT)	L42293	166.4	640.2	2.1	3.84736
L08493	AAC42032	NP_000800	NM_000809	79	GABA-A receptor alpha-4 subunit gene, complete cds		272.9	615.6	2.1	2.25577
L25866	AAA40768	AAA59978	M36718	66	octamer-binding transcription factor		381.4	791.9	2.1	2.0763
M64092	AAA41879	NP_115860	NM_032471	33	protein kinase inhibitor		371.8	785.1	2.1	2.11162
M80784	AAA42236	NP_003234	NM_003243	79	type III TGF-beta receptor		380.7	805	2.1	2.11453
U01344	P50297	g2245376	U80835	76	A-2 arylamine N-acetyltransferase		712.3	835.4	2.1	1.17282
U37462	AAC52320	XP_038238	XM_038238	98	MEK5alpha-1.		785.6	1637.9	2.1	2.0849
U93306	AAB97508	AAB88005	AF035121	83	VEGF receptor-2/FLK-1		335.8	570.6	2.1	1.69923
X57970	CAA41036	XP_051651	XM_051651	65	connexin 46		440	942.7	2.1	2.1425
NC_001665					mitochondrial genome	AA799594	242.6	528.8	2	2.17972
AA799600	P43035	S36113	L13388	33	ESTs, Weakly similar to PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB ALPHA SUBUNIT [R.norvegicus]		302.5	592.3	2	1.95802
AA799686					EST(not recognised)		149.6	766.5	2	5.12366
NM_020616	NP_065641	NP_065693	NM_020642	70	Mus musculus predicted gene ICRFP703B1614Q5.6	AA799992	286.1	569.4	2	1.99021
AA800186					EST (not recognized)		394	791.4	2	2.00863

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

AA875362					EST (not recognized)		893.9	834.4	2	0.93344
NM_022548	NP_071993	NP_071915	NM_022470	87	p53-activated gene 608	AA875455	589	1202.8	2	2.04211
AF262320	AAK58519	XP_029519	XM_029519	88	apoptosis-inducing factor	AA891591	105.7	1616.6	2	15.2942
AA891759					Mus musculus 8 days embryo cDNA, RIKEN		384.9	778.9	2	2.02364
AA893307					EST(not recognised)		311.6	981	2	3.08408
AF016048	AAC27974	NP_002563	NM_002572	99	platelet-activating factor acetylhydrolase alpha 2 subunit	AA899935	411.3	840.6	2	2.04376
AB004831	BAA25652	AAB24822	S52229	63	B29/Ig-beta/CD79b		816.4	1595.6	2	1.95443
AB011666	BAA25724	NP_009055	NM_007124	96	utrophin		700.2	1407.7	2	2.01043
AF052596	AAC06031	XP_031741	XM_031741	87	SNAP-23		618.2	1210.4	2	1.95794
AI070295	S68690	P24522	L24498	92	DNA-damage-inducible transcript 1		600.5	1021.2	2	1.70058
D13211	BAA02498	NP_000824	NM_000833	94	N-methyl-D-aspartate receptor subunit		138.1	546.3	2	3.95583
D37884	BAA07126	NP_001268	NM_001277	47	choline kinase R		411.9	817.3	2	1.98422
D50558	BAA23470	XP_032680	XM_032680	56	Membrane glycoprotein		245.1	530.5	2	2.16442
NM_017017	NP_058713	XP_052255	XM_052255	87	hepatocyte growth factor (scatter factor)	E03190	602.7	501.8	2	0.83259
J02679	AAA41715	NP_000894	NM_000903	82	NAD(P)H:menadione oxidoreductase		2930	5955.3	2	2.03253
J04187	A31887	Q16696	U22028	67	Cytochrome P450 IIA2 (see 257 on this sheet)		158.3	839.1	2	5.30069
K02423	AAA98533	XP_030823	XM_030823	85	myosin light chain		4891.2	9714.9	2	1.9862
L01624	AAA42137	XP_037046	XM_037046	91	serine/threonine protein kinase		1052.3	2115.2	2	2.01007
L32601	P51652	P42330	D17793	71	20-alpha-hydroxysteroid dehydrogenase (20-alpha-HSD)		584.9	1476.6	2	2.52453
M16853	AAA42207	AAA60627	M15565	55	T-cell receptor alpha-chain C-region precursor	L37966	835.9	1125.8	2	1.34681
M27151	AAA41636	NP_002460	NM_002469	79	muscle regulatory factor MRF4.		328.3	669.7	2	2.0399
M77694	AAA41142	NP_000128	NM_000137	86	fumarylacetoacetate hydrolase (FAH)		371.5	759.4	2	2.04416
M84719	P36365	Q01740	M64082	82	Flavin-containing monooxygenase 1		463.5	924.2	2	1.99396
S76742	AAB32806	NP_064593	NM_020208	84	neurotransmitter transporter rB21a		825.6	1677.3	2	2.03161
U04835	1921368A	XP_005813	XM_005813	100	cAMP responsive element modulator		248.7	673.7	2	2.70889
U28938	T14328	S60613	Z48541	89	Receptor-type protein tyrosine phosphatase D30		259	822.5	2	3.17568
U96921	AAB72152	NP_003857	NM_003866	85	Inositol polyphosphate 4-phosphatase type II-beta		393.1	800.7	2	2.03689
X73371	Q63203	g29428	X52473	54	Fc gamma receptor		218.1	607.4	2	2.78496

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

X16957	CAA34831	NP_000090	NM_000099							
				72	cysteine proteinase inhibitor cystatin C	AI231292	33265.6	65579.4	2	1.97139
M11794	AAA41640		No Human		metallothionein	AI176456	3073.2	6117.4	2	1.99056
AA686870					EST(not recognised)		372	698.5	1.9	1.87769
NM_019734	NP_062708	NP_004306	NM_004315		N-acylsphingosine amidohydrolase; acid					
				79	ceramidase	AA800082	1569.8	1962.8	1.9	1.25035
AA866299					EST(not recognised)		366.8	691.8	1.9	1.88604
AA874990		XP_035810	XM_035810		ESTs, Weakly similar to T25404 hypothetical protein T28C6.1					
				91	[C.elegans]		950.9	1764.5	1.9	1.85561
X73683	CAA52035	XP_011165	XM_011165	97	histone H3	AA875069	1432.5	2670	1.9	1.86387
AA875090		NP_060065	NM_017595							
				90n	I-kappa-B-interacting Ras-like protein 2		1096.2	2106.1	1.9	1.92127
AA875615					Mus musculus 10 days embryo cDNA, RIKEN		586.8	1103.7	1.9	1.88088
AA891255					EST(not recognised)		457.9	841.1	1.9	1.83686
AA891476					Mus musculus adult male corpus striatum cDNA, RIKEN		469	905.9	1.9	1.93156
AA892149					EST(not recognised)		201.8	1523.4	1.9	7.54906
AA892754					EST(not recognised)		399.4	768.1	1.9	1.92313
AA892779					EST (not recognized)		331.6	644.4	1.9	1.94331
M31788	AAA41838	NP_000282	NM_000291	97	phosphoglycerate kinase	AA892797	6621.7	12391.7	1.9	1.87138
AA893000					Human DNA sequence from clone RP11-125A7		684.9	1303.7	1.9	1.90349
AA893592	Q62703	Q15293	D42073		ESTs, Weakly similar to RETICULOCALBIN 2 PRECURSOR					
				94	[R.norvegicus]		383.4	794.6	1.9	2.07251
AA893970					Homo sapiens cDNA FLJ14265 fis, clone PLACE1002256		443	862.2	1.9	1.94628
AB015042	BAA28746	NP_004386	NM_004395	64	drebrin		1202.5	2335.5	1.9	1.9422
AF031430	AAC17131	XP_004526	XM_004526	84	Syntaxin 7		740.3	1382.4	1.9	1.86735
AF048828	AAD02476	MMHUP3	L06132	93	Voltage-dependent anion channel 1		1267.4	2429.8	1.9	1.91715
AF077354	Q63617	P34932	AB023420		Ischemia responsive 94 kDa protein					
				95	(irp94)		685.6	1101	1.9	1.60589
AF091573	AAC64594	NP_003544	NM_003553	66	HGL-SL2 olfactory receptor		807.7	1517.3	1.9	1.87854
AF092450	AAC62110	NP_005447	NM_005456		Rattus norvegicus JIP-1b mRNA,					
				80n	complete cds		1684.1	3277.8	1.9	1.94632
NC_001665					mitochondrial genome	AI010632	50854.7	101748	1.9	2.00866

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

AI045558	JE0155	XP_049282	XM_049282	90	Translocator of inner mitochondrial membrane 44		1037.4	1944.4	1.9	1.8743
U31866					Nclone10	AI071866	481.4	1243	1.9	2.58205
AI231778					Mus musculus adult male liver cDNA, RIKEN		431.1	813.8	1.9	1.88773
X80899	CAA56861	XP_002700	XM_002700	88	cytochrome C oxidase subunit VII homologue	AI232307	3738.1	7251.9	1.9	1.94
M12894	AAA41289		No Human		putative glutathione S-transferase Ya subunit	AI235747	1201.7	1818.2	1.9	1.51302
AI638988					EST(not recognised)		1392.2	2617.2	1.9	1.8799
AI639105					Mus musculus adult male urinary bladder cDNA, RIKEN		377.7	1111.1	1.9	2.94175
AI639345					EST (not recognized)		1498.5	2879.1	1.9	1.92132
AI639477					EST(not recognised)		317	1864.1	1.9	5.88044
AJ006710	CAA07199	NP_002638	NM_002647	88	phosphatidylinositol 3-kinase		636.7	1867.2	1.9	2.93262
D16309	BAA03816	NP_001751	NM_001760	80	Cyclin D3		1650.2	3117.2	1.9	1.88898
D83538	BAA19614	P42356	L36151	98	Phosphatidylinositol 4-kinase		294	555.6	1.9	1.8898
J04943	AAA40794	AAH12566	BC012566	78	nucleolar protein B23.2		724.3	1395.4	1.9	1.92655
J05132	AAA42315	AAG30420	AF297093	78	truncated UDP-glucuronosyltransferase		778.4	1443.6	1.9	1.85457
L11587	AAC37656	XP_016527	XM_016527	65	Rat leukocyte common antigen-related phosphatase (LAR-PTP2)		847.2	2168.9	1.9	2.56008
L15619	P13862	P13862	X16937	100	Casein kinase II beta subunit		378	726.9	1.9	1.92302
L16764	AAA17441	AAA52697	M11717	87	Heat shock protein 70-1		638.3	1244.3	1.9	1.9494
L22180	AAA19818	NP_000322	NM_000331	70	amyloid A		387.2	717.7	1.9	1.85356
L47281	AAB72238	NP_000082	NM_000091	91	Rattus norvegicus alpha-3 type IV collagen (COL4A3) mRNA, partial cds		484.8	1386.2	1.9	2.85932
M31837	AAA41383	XP_038124	XM_038124	76	Insulin-like growth factor binding protein		287.3	867.9	1.9	3.02088
M34134	P18342	P09493	M19713	94	Tropomyosin 1 (alpha)		27548.1	45330.1	1.9	1.64549
M55532	AAA40892	NP_056532	NM_015717	37	carbohydrate-binding receptor		344.7	642.1	1.9	1.86278
U07971	AAA21250	NP_001473	NM_001482	90	L-arginine:glycine amidinotransferase		429.6	835.3	1.9	1.94437
U09815	AAA56870	NP_001703	NM_001712	31	pregnancy-specific glycoprotein		501.4	977.3	1.9	1.94914
U34932	AAA79137	NP_079092	NM_024816	76	Fos-related antigen		2030.1	3766.4	1.9	1.85528
U40001	AAC52771	XP_008882	XM_008882	65	hormone-sensitive lipase testicular isoform		1327.1	5232.6	1.9	3.94288

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

U49099	AAC52597	AAD12945	AF073926	98	Golgi SNAP receptor complex member 1		2429.5	4625.6	1.9	1.90393
U52104	AAB03282	NP_001378	NM_001387	94	rCRMP-4		287.8	556.2	1.9	1.93259
U64689	AAB40631	AAB40661	U69140	84	Rattus norvegicus zygin-related protein type II (Zrp2) mRNA, partial cds		386.5	750.5	1.9	1.94179
U89744	g1890275	P24928	X63564	30	Rat putative cell surface antigen		631	1183.6	1.9	1.87575
U94708	AAB53325	XP_007322	XM_007322	59	EP2 prostanoid receptor		668.5	855.7	1.9	1.28003
X55446	CAA39087	NP_000760	NM_000769	58	Rat mRNA for cytochrome P-450 (CYP2C23)		364.4	689.1	1.9	1.89105
X62839	CAA44643	CAC19684	AL137790	54	Voltage-gated potassium channel		397.9	747	1.9	1.87736
X65083	P80299	P34913	L05779	78	Cytosolic epoxide hydrolase		512.5	979	1.9	1.91024
X89703	CAA61850	CAA61822	X89675	46	TPCR19 protein		872	1620.7	1.9	1.8586
X96488	CAA65342	XP_010067	XM_010067	93	SAP kinase-3		833.9	1577.4	1.9	1.89159
Z13993	CAA78384	NP_001891	NM_001900	31	prostatic 22kDa glycoprotein		32.6	621.5	1.9	19.0644
Z14118	CAA78488	NP_006197	NM_006206	81	platelet-derived growth factor receptor alpha,extracellular domain		85.7	750.6	1.9	8.75846
Z36276	Q64595	JE0103	Y16105	96	cGMP dependent protein kinase type II		515.1	992.9	1.9	1.92759
AA799711	S12207		No Human		ESTs, Moderately similar to S12207 hypothetical protein [M.musculus]		453.1	563.7	1.8	1.2441
AA799891					EST(not recognised)		375.3	823.4	1.8	2.18398
AA800216					Mus musculus 18 days embryo cDNA, RIKEN		71.4	1266.8	1.8	17.7423
NM_031971	NP_114177	AAA52697	M11717	87	Heat shock protein 70-1 (Hspa1a),	AA818604	184.1	754.7	1.8	4.0994
AF148511	AAD39515	NP_006858	NM_006867	84	hermes	AA859519	1349.6	1979.8	1.8	1.46695
AA859897					Human chromosome 14 DNA sequence BAC R-299L17		709.4	2402.9	1.8	3.38723
AA874873					Mus musculus, clone MGC:7182 IMAGE:3481673		1172	2059.2	1.8	1.757
AA874887	CAA06377	BAA73535	AB019987	100	ESTs, Weakly similar to SMC-protein [R.norvegicus]		395	699.2	1.8	1.77013
AA891931					EST(not recognised)		489.2	1218.4	1.8	2.4906
AA891943					EST (not recognized)		1283.2	2298.7	1.8	1.79138
NM_020558	NP_065583	NP_006324	NM_006333	90	nuclear DNA-binding protein (C1d-pending),	AA891969	522.9	606.1	1.8	1.15911
AA892299					EST(not recognised)		838.3	1487.3	1.8	1.77419
NM_022521	NP_071966	NP_000265	NM_000274	87	ornithine aminotransferase	AA893325	1885.3	3340.9	1.8	1.77208

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

AA893495	P31211	A28321	J02943	56	ESTs, Highly similar to CORTICOSTEROID-BINDING GLOBULIN PRECURSOR [R.norvegicus]		59.9	847.6	1.8	14.1503
AA893662					EST(not recognised)		603.2	786.3	1.8	1.30355
AA894148					Mixed cDNA - Apolipoprotein A-IV / 28S ribosomal RNA		14609.1	26204.2	1.8	1.79369
X68394	CAA48460	NP_002515	NM_002524	94	N-ras gene for p21	AA943331	417.6	1018.9	1.8	2.43989
AB012933	O88813	JX0202	D10040	62	Acyl-CoA synthetase 5		1046.4	1200.6	1.8	1.14736
AF015953	AAC21449	XP_031166	XM_031166	89	TIC		212.1	957.8	1.8	4.51579
AF023657	AAB86925	NP_078917	NM_024641	88	endo-alpha-D-mannosidase (Enman)		371.5	684.4	1.8	1.84226
NM_021754	NP_068522	NP_057018	NM_015934	92	Nopp140 associated protein	AF069782	1094.9	2013.2	1.8	1.83871
AF075382	AAC26222	NP_003868	NM_003877	87	suppressor of cytokine signaling-2		356.9	872.4	1.8	2.44438
AF100470	AAC72398	NP_055260	NM_014445	100	ribosome attached membrane protein 4		1014	1791	1.8	1.76627
AF106563	AAC83936	NP_005680	NM_005689	78	Rattus norvegicus mRNA for ABC transporter		525.3	944.4	1.8	1.79783
NM_017278	NP_058974	NP_002777	NM_002786	97	proteasome	AI009111	659.4	1195.6	1.8	1.81316
AI009268	P15791	Q13557	AF071569	92	Ca++/calmodulin-dependent protein kinase II, delta subunit		415.1	607.8	1.8	1.46423
AI044716	P47971	Q15818	U61849	95	Rattus norvegicus neuronal pentraxin precursor mRNA, complete cds		946.6	1428.4	1.8	1.50898
NM_017279	NP_058975	NP_002777	NM_002786	97	proteasome	AI170403	1724	3184.4	1.8	1.8471
AI639026					EST(not recognised)		764.7	559.8	1.8	0.73205
U91922	AAC05725	NP_001348	NM_001357	83	RNA helicase A (Ddx9)	AI639188	825.6	1484.8	1.8	1.79845
X59859	CAA42519	NP_001911	NM_001920	74	decorin	AI639233	3531.9	6351.8	1.8	1.79841
AJ000347	CAA04022	NP_006076	NM_006085	91	3'(2'),5'-bisphosphate nucleotidase		422.1	1387.2	1.8	3.28643
AJ007632	CAA07591	XP_008403	XM_008403	61	ELK channel 3 (Potassium channel)		1821.8	3265.1	1.8	1.79224
D13907	S36390	O75439	AF054182	88	Mitochondrial processing peptidase beta		586.6	1034.7	1.8	1.76389
D26178	BAA05166	NP_055735	NM_014920	79	serine/threonine protein kinase		681.8	1196.2	1.8	1.75447
D28560	BAA05910	NP_006200	NM_006209	88	phosphodiesterase I		568.2	1263.9	1.8	2.22439
D49708	BAA08556	AAC28242	U61267	100	Rattus norvegicus mRNA for RNA binding protein (transformer-2-like), complete cds	AI231164	1149.2	2067.3	1.8	1.7989
D90048	BAA14101	NP_001669	NM_001678	100	Na+,K+ -ATPae beta2 subunit		1646	3020.2	1.8	1.83487
E00898		CAA52817	X74818	86	Cancer specific cDNA	E00898	1061.9	2717.4	1.8	2.559

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

J02827	AAA40811	NP_000700	NM_000709	86	branched chain alpha-ketoacid dehydrogenase		580.2	2199.2	1.8	3.79042
K01932	AAA41294	NP_000838	NM_000847	75	glutathione S-transferase Yc subunit		1863	3378.2	1.8	1.81331
L05435	AAA42188	NP_055664	NM_014849	84	synaptic vesicle protein (SV2)		1180.9	1858.9	1.8	1.57414
L08495	AAC42034	NP_000802	NM_000811	86	GABA-A receptor alpha-6 subunit		537.9	1444.3	1.8	2.68507
L24207	AAA41023	NP_000767	NM_000776	68	Testosterone 6-beta-hydroxylase (CYP3A1)		610.9	798.6	1.8	1.30725
M11670	AAA40884	NP_001743	NM_001752	88	catalase		1087.6	1766.7	1.8	1.6244
M27433	AAA60735	CAA43011	X60481	100	histone H4.		744.8	935.4	1.8	1.25591
M27440	AAA74690	NP_000375	NM_000384	53	apolipoprotein B.		673.4	1191.9	1.8	1.76997
NM_012632	NP_036764	XP_012244	XM_012244	94	Proline-rich protein, salivary	M83567	539.8	1237.3	1.8	2.29215
M96375	B40228	NP_004792	NM_004801	76	Non-processed neurexin I-beta		1697.9	3085.1	1.8	1.81701
S39221	AAB22435	NP_067544	NM_021569	96	NMDA receptor		1071.7	1897.9	1.8	1.77092
S58528	AAB26277	NP_002201	NM_002210	91	Integrin, alpha V		881.5	867.2	1.8	0.98378
S76758		BAB55545	AB038670	95n	BDNF=brain-derived neurotrophic factor (alternatively spliced)		1502.8	2742.7	1.8	1.82506
S79304	AAB21298		No Human		Rattus sp. cytochrome oxidase subunit I mRNA, partial cds; and tRNA-Ser gene, complete sequence; mitochondrial genes for mitochondrial products		40182.4	71690.7	1.8	1.78413
U10897	AAA64638	NP_036254	NM_012122	70	kidney microsomal carboxylesterase		431.5	1466.2	1.8	3.39791
U12568	AAA50861	NP_004302	NM_004311	89	ADP-ribosylation factor-like protein 3		735.9	1308	1.8	1.77742
U17837	AAA74468	NP_036363	NM_012231	67	zinc finger protein RIZ		533.8	942.2	1.8	1.76508
U27518	g1177818	g3287473	U59209	62	UDP-glucuronosyltransferase		510	909	1.8	1.78235
U32498	AAC52265	NP_068579	NM_021807	94	rsec8		295	1475.8	1.8	5.00271
U40628	S70009	AAC34993	AF043244	81	Unknown Glu-Pro dipeptide repeat protein		86.8	898.2	1.8	10.3249
U49953	AAB61533	XP_034970	XM_034970	92	protein kinase MUK2		20	651.5	1.8	32.575
U50353	AAC99551	NP_066290	NM_021010	35	defensin 3a (RatNP-3a)		3548.3	6373.5	1.8	1.79621
U50717	AAC52643	XP_012060	XM_012060	88	Synaptic density protein PSD-93 mRNA, partial cds		470.9	847.2	1.8	1.79911
U56862	Q62981	Q15072	X70394	80	Pancreas zinc finger protein		362.6	667	1.8	1.83949
U73142	AAC71059	XP_043351	XM_043351	94	p38 mitogen activated protein kinase		1560.6	4054.8	1.8	2.59823
U75916	g1839162	g5924408	AF177533	88	Zonula occludens 2 protein (ZO-2)		969.3	1707.2	1.8	1.76127
U75921					APC binding protein EB1		20	1482.3	1.8	74.115
X01785	CAA25925	NP_005935	NM_005944	69	MRC OX-2 antigen		1240	1147.5	1.8	0.9254
X06832	CAA29988	NP_001266	NM_001275	53	Prechromogranin A		3133.2	5607.4	1.8	1.78967

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

X56747	CAA40069	NP_002290	NM_002299	76	Rat mRNA for fetal intestinal lactase-phlorizin hydrolase		1734.1	1246.8	1.8	0.71899
X60769	CAA43179	NP_005185	NM_005194	53	SF-B (silencer factor B)		587.2	1073.9	1.8	1.82885
X98377	CAA67023	NP_000108	NM_000117	61	Emerin		4552.3	8087.3	1.8	1.77653
X99338	CAA67712	NP_036560	NM_012428	92	Glycoprotein 65		3235.6	5760.7	1.8	1.78041
Y17295	g2317735	P30041	D14662	91	Rattus norvegicus mRNA for thiol-specific antioxidant protein (1-Cys peroxiredoxin		494.7	891.7	1.8	1.80251
AI639324					Homo sapiens clone SP329 unknown mRNA		406.9	749.2	1.8	1.84124
AA799539		NP_005997	NM_006006	35	ESTs, Weakly similar to 2118318A promyelocyte leukemia Zn finger protein [M.musculus]		1374.2	2377.7	1.7	1.73024
AA799645	O08589	O00168	U72245	80	FXYD domain-containing ion transport regulator 1		14627.8	25099.7	1.7	1.71589
AA799741		XP_005981	XM_005981	85n	suppressor of var1 (S.cerevisiae) 3-like 1 [Homo sapiens].		337.2	580.4	1.7	1.72123
AA799812		XP_005386	XM_005386	84n	protein tyrosine phosphatase, non-receptor type 3 (PTPN3),		577.7	860	1.7	1.48866
AA800290					EST (not recognized)		758.9	819.3	1.7	1.07959
AA800699		XP_028517	XM_028517	91n	ESTs, Weakly similar to YN60_YEAST HYPOTHETICAL 32.3 KDA PROTEIN IN KRE1-HXT14 INTERGENIC REGION [S.cerevisiae]		480.7	803.1	1.7	1.67069
AA800719		XP_043341	XM_043341	87n	KIAA1181 protein		1840.2	3544	1.7	1.92588
AA817843					Mus musculus ES cells cDNA, RIKEN		446.8	769.9	1.7	1.72314
AA866472	2008109A	S40510	M86667	97	Nucleosome assembly protein 1-like 1		451.6	946.7	1.7	2.09632
AA875192	NP_079642		No Human		Rat EST; mouse hypothetical protein from a Riken		769.7	1324.3	1.7	1.67697
AA891499			AC008462	86n	Homo sapiens chromosome 5 clone CTC-352J10, complete sequence		2016.4	3431.9	1.7	1.70199
NM_013119	NP_037251	XP_008249	XM_008249	64	Sodium channel, voltage-gated, type III, alpha polypeptide (Scn3a)	AA891751	2019.6	2311.1	1.7	1.14434
AA891790					Mus musculus adult male tongue cDNA, RIKEN		1293.4	2244.1	1.7	1.73504
AA891938					Mus musculus adult male lung cDNA, RIKEN		459.5	609.2	1.7	1.32579
AA892296					Mus musculus chromosome 11, clone RP23-196F5		485.5	1130	1.7	2.3275

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

AF321130	AAK11183	NP_001518	NM_001527	67	histone deacetylase 2	AA892297	1431.6	2501.8	1.7	1.74756
AA892538					EST (some homology with mouse chromosomal)		441.9	1343.6	1.7	3.04051
L12458	AAA41552	NP_000230	NM_000239	64	lysozyme	AA892775	13049.9	22753.7	1.7	1.74359
AA892854		O43927	AF044197		ESTs, Weakly similar to B LYMPHOCYTE CHEMOATTRACTANT					
				40	PRECURSOR [M.musculus]		389.2	675.9	1.7	1.73664
AA892993	AAF66708	XP_047641	XM_047641		Mus musculus HMG domain protein					
				73	HMGX2 (Hmgx2)	AA892993	1198.6	2026.7	1.7	1.69089
AA893172					EST (not recognized)		276.3	756.5	1.7	2.73797
AA893328	P35565	P27824	L10284		ESTs, Highly similar to CALX RAT CALNEXIN PRECURSOR					
				84	[R.norvegicus]		822.7	1410	1.7	1.71387
AA893870			M11167	95n	28S ribosomal RNA gene (2 on d.s.)		10882.1	18663.1	1.7	1.74714
AA893871					EST(not recognised)		453.6	1166.4	1.7	2.57143
L09752	AAA41010	NP_001750	NM_001759	88	cyclin D2 (VIN1)	AA899106	1167.7	2028.2	1.7	1.73692
D29683	BAA06152	XP_033687	XM_033687	90	endothelin-converting enzyme.	AA956930	433.5	721.3	1.7	1.6639
AA957961	P18395	BAA74908	AB020692		Rat unr mRNA for unr protein with					
				98	unknown function		1056.1	1754.7	1.7	1.66149
AB001453	BAA28174	NP_058544	NM_016848	82	N-Shc		1339.8	5515.9	1.7	4.11696
AB009463	BAA32331	BAA32330	AB009462	84	LRp105		356.2	613.1	1.7	1.72122
AF015304	O54698	Q99808	AF079117		Solute carrier family 29 (nucleoside					
				78	transporters), member 1		937.7	1614.2	1.7	1.72145
AF020210	AAB71235	XP_050175	XM_050175	83	DLP1 splice variant 4		1001.5	2948.7	1.7	2.94428
AF041107	P49816	T08722	XM_046659	92	Tulip 1		645.3	1123.7	1.7	1.74136
AF041373	AAB97078	NP_009097	NM_007166		Clathrin assembly protein short form					
				87	(CALM)		3102.1	5233.2	1.7	1.68699
AF062594	2008109A	S40510	M86667							
				97	Nucleosome assembly protein 1-like 1		420.6	915.7	1.7	2.17713
AF072439	O88553	Q9Y6Q3	AF022158		Rattus norvegicus zinc-finger protein-37					
				70	mRNA, complete cds		1103.8	1850.2	1.7	1.67621
AF080568	P19836	Q99447	D84307		Phosphate cytidylyltransferase 2,					
				88	ethanolamine		1664.1	2812.3	1.7	1.68998
AF082533	AAC69890	NP_004820	NM_004829	63	NK receptor KILR-1 (KILR-1)		542.7	1501.9	1.7	2.76746
AF090692	AAC36317	NP_005483	NM_005492		Cystatin-related epididymal spermatogenic protein (CRES) mRNA,					
				62	complete cds		813.8	1356	1.7	1.66626
AF091575	AAC64595	NP_006628	NM_006637	48	HFV-FD1 olfactory receptor		742.3	1283.9	1.7	1.72962

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

AF096835	AAC83801	NP_004827	NM_004836	77	Rattus norvegicus pancreatic eukaryotic initiation factor 2 alpha-subunit kinase (PEK) mRNA		926.6	1534	1.7	1.65551
M27315	AAB00991		No Human		cytochrome c oxidase subunit I	AI010292	76787.6	127842	1.7	1.66488
AI072435	A23677	I39382	J03827	97	Y box protein 1		792.3	1349.9	1.7	1.70377
NM_031099	NP_112361	NP_000960	NM_000969	92	ribosomal protein L5 (Rpl5),	AI103498	666.8	567.4	1.7	0.85093
AI145494	D30411	JC4940	U40215	94	Synapsin II		610	1035.3	1.7	1.69721
AI178267		XP_044466	XM_044466	93n	Homo sapiens membrane protein CH1		617.2	1079.1	1.7	1.74838
AI228407	P13589	I84638	X60435	82	Pituitary adenylate cyclase activating polypeptide (41 on d.s.)		410	935.8	1.7	2.28244
AY028804	AAK83555	NP_067021	NM_021198	98	golli-interacting protein	AI229655	1774.8	3002.7	1.7	1.69185
AI229924	NP_080263	XM_010025	XP_010025	87n	ESTs, Moderately similar to NB4M_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE B14 SUBUNIT [H.sapiens]		1650.4	2865.3	1.7	1.73612
AI231354	P49186	P45984	L31951	98	Stress activated protein kinase alpha II		431.8	754.3	1.7	1.74687
AI234939					Mus musculus RIKEN cDNA 1500035H01 gene		1558.3	2720.9	1.7	1.74607
M12492	AAA42047	XP_004959	XM_004959	91	type II cAMP-dependent protein kinase regulatory subunit	AI235758	1186.4	2780.4	1.7	2.34356
AI639004					Homo sapiens mRNA; cDNA DKFZp434F1626		1203.8	2049.8	1.7	1.70277
AI639020					Mus musculus, clone MGC:11798 IMAGE:3595439		464.3	969.7	1.7	2.08852
AI639176					EST (not recognized)		796.2	1801.7	1.7	2.26287
AI639241					Mus musculus adult male testis cDNA, RIKEN		1546.3	2611.7	1.7	1.689
AI639411					Mus musculus, clone MGC:6389 IMAGE:3583081		490.9	575.1	1.7	1.17152
AI639425					EST(not recognised)		1137.8	1578.2	1.7	1.38708
AI639434					EST (not recognized)		901.9	1543.1	1.7	1.71094
AI639471					EST (not recognized)		1802.7	4993.3	1.7	2.7699
AF093576	AAC61874	AAB41498	U83867	51	erythroid alpha-spectrin	AI639523	480.1	833	1.7	1.73506
D10853	P35433	Q06203	D13757	93	Amidophosphoribosyltransferase		952.6	1609.5	1.7	1.68959
D12769	BAA02236	NP_001197	NM_001206	91	BTE binding protein		1318.4	3559.4	1.7	2.69979
D25543	BAA05026	CAA53052	X75304	64	Novel golgi-associated protein GCP360		527.1	910.2	1.7	1.72681

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

D26154	BAA05141	XP_032627	XM_032627	82	RB109 (brain specific protein)		2099.7	3648.7	1.7	1.73772
D44481	BAA07924	AAH08506	BC008506	92	CRK-II		1184.3	4019.8	1.7	3.39424
D78613	BAA11433	XP_005781	XM_005781	80	Protein tyrosine phosphatase epsilon M		1624.6	2765.3	1.7	1.70214
NM_030656	NP_085914	NP_000021	NM_000030	76	Serine-pyruvate aminotransferase	E01050	1570.5	2674.4	1.7	1.7029
H31859					EST(not recognised)		675.1	1404.1	1.7	2.07984
NM_017014	NP_058710	XP_002155	XM_002155	79	glutathione-S-transferase, mu type 2	H32189	3729.9	6538.7	1.7	1.75305
J02749	AAA41497	NP_001598	NM_001607	83	peroxisomal 3-ketoacyl-CoA thiolase precursor		694.7	1192.8	1.7	1.717
J02998	AAA42006	NP_004152	NM_004161	99	ras protein		1446.4	2501.1	1.7	1.72919
J04591	AAA41096	AAA52308	M80536	81	Dipeptidyl peptidase IV		743.7	1246.5	1.7	1.67608
L34049	AAA51369	NP_004516	NM_004525	73	megalin		1970.4	2314.2	1.7	1.17448
M22400	AAA41735	NP_004475	NM_004484	88	developmentally regulated intestinal protein (OCI-5)		1290.5	2707	1.7	2.09764
M27467	AAA79270	NP_004365	NM_004374	64	Heart cytochrome oxidase subunit VIc (COX-VIc)		3759.4	6488.1	1.7	1.72583
M31038	AAA41608		No Human		MHC non-RT1.A alpha-1-chain protein precursor		624.9	1091.4	1.7	1.74652
M33936	AAA41458	NP_000769	NM_000778	73	cytochrome P450 (IVA3)		559.2	925.3	1.7	1.65469
M58287	AAA41726	XP_038856	XM_038856	83	Rat non-specific lipid transfer protein (nsL-TP) mRNA, 3' end		454	755.1	1.7	1.66322
M64391	AAA41754	NP_003544	NM_003553	56	Olfactory protein mRNA	AF091574	557	970.9	1.7	1.74309
M69055	AAA42019	NP_002169	NM_002178	66	IGFBP-6		8553.8	14283.1	1.7	1.6698
M73049	AAA41444	NP_116116	NM_032727	71	alpha-internexin		1289.7	3230.7	1.7	2.505
M91652	AAC42038	NP_002056	NM_002065	91	glutamine synthetase		2983	4967	1.7	1.6651
S68736	AAB29713	XP_052590	XM_052590	80	Myosin heavy chain mRNA		2188.2	3759.5	1.7	1.71808
M96578	AAA41303	NP_002967	NM_002976	86n	voltage-dependent sodium channel alpha subunit	S75991	9546.1	18710.4	1.7	1.96
U16686	AAA91974	NP_066290	NM_021010	43	defensin RatNP-1 precursor		1918.2	3276.7	1.7	1.70822
U18762	AAB07997	NP_003699	NM_003708	71	retinol dehydrogenase type I		62.7	647.1	1.7	10.3206
U22321	AAC52202	XP_049422	XM_049422	89	casein kinase 1 gamma 3 isoform		436.2	1054.4	1.7	2.41724
U31159	AAC99858	AAD15418	AC004912	78	CR16		320.6	1012.8	1.7	3.15908
U35774	AAC52385	NP_005495	NM_005504	72	cytosolic branch chain aminotransferase		8454.7	14456.1	1.7	1.70983
U44129	AAC52434	NP_005561	NM_005570	81	p58		709.7	1205.6	1.7	1.69875
U44948	Q62908	Q16527	U46006	98	Smooth muscle cell LIM protein (SmLIM)		1735.1	2997.2	1.7	1.72739
U50736	A44437	A57291	X83703	90	Cardiac ankyrin repeat protein		486.9	813.8	1.7	1.67139

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

U59240	AAC52854	NP_055363	NM_014548	89	N-tropomodulin		1525.2	2572.8	1.7	1.68686
U78517	AAD03423	XP_002437	XM_002437	95	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor II (cAMP-GEFII) mRNA, partial cds		489.7	813.4	1.7	1.66102
U81186	AAD00504	NP_057226	NM_016142	83	Smooth muscle-specific 17 beta-hydroxysteroid dehydrogenase type 3		921.3	1562.5	1.7	1.69597
U92803	AAB61572	NP_001287	NM_001296	58	CC-chemokine-binding receptor JAB61		643	1065.7	1.7	1.65739
X53231	CAA37323		No Human		put. preoptic regulatory factor-1		881.5	1468.2	1.7	1.66557
X55572	CAA39158	NP_001638	NM_001647	74	apolipoprotein D		29173.3	50377.6	1.7	1.72684
X59859	CAA42519	NP_001911	NM_001920	74	decorin	AI639233	24475.2	41608.1	1.7	1.70001
X63410	CAA45007	AAB23169	S43859	59	Hydroxysteroid sulfotransferase		788.5	1307	1.7	1.65758
X79208	CAA55797	AAK38351	AY029770	60	CCK(B)		3326.2	5716.2	1.7	1.71854
NM_012826	NP_036958	NP_001176	NM_001185	59	zn - alpha2 - glycoprotein	X86178	1109.1	1892.6	1.7	1.70843
X89701	CAA61848	XP_036497	XM_036497	71	TPCR13 protein		20	723	1.7	36.15
Y17048	MCRT	NP_112482	NM_031205	98	Rattus norvegicus mRNA for calcendrin		4430.4	9782.2	1.7	2.20797
Z12158	CAA78146	NP_000275	NM_000284	95	Pyruvate dehydrogenase E1 alpha form 1 subunit		4699.1	7933.9	1.7	1.68839
Z35654	Q63406	BAA20817	AB002360	88	R.norvegicus mRNA for Ost oncogene		572.9	949.6	1.7	1.65753
Z46614	CAA86587	XP_004967	XM_004967	95	caveolin		1520.1	2524.5	1.7	1.66075
D87839	BAA25570	XP_007904	XM_007904	90	beta-alanine oxoglutarate aminotransferase		403.5	676.2	1.7	1.67584
NM_013559	NP_038587	BAA34780	AB003334	89	heat shock protein, 105 kDa; HSP105 42 C-HSP	AA108277	2967.8	3732.6	1.6	1.2577
NM_012032	NP_036162	NP_006802	NM_006811	71	tumor differentially expressed 1	AA799641	1797.9	3379.3	1.6	1.87958
AA799751					EST(not recognised)		1657.3	2393.5	1.6	1.44422
AA800126		CAC11116	AL357374	93n	Human DNA sequence from clone RP11-353C18 on chromosome 20		911.4	1499.2	1.6	1.64494
AA800597					EST (not recognized)		1276.9	2585.3	1.6	2.02467
AA800851		NP_006234	NM_006243	89	protein phosphatase 2, regulatory subunit B (B56)		1548.4	2539.5	1.6	1.64008
AF062644	AAC16448	XP_052680	XM_052680	71	vascular endothelial growth factor	AA850734	678.2	1073.5	1.6	1.58287
AA859468					EST (not recognized)		496.6	1002.1	1.6	2.01792
AA859520					Mus musculus 18 days embryo cDNA, RIKEN		1118.1	1783.1	1.6	1.59476
AA859911	Q11205	JC5251	U63090	93	Sialyltransferase 5		479.4	759.9	1.6	1.58511

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

Y17793	CAA76850	BAB13394	AB046788	52	Dutt1	AA860017	688.6	869	1.6	1.26198
AA866293					EST(not recognised)		843.7	1320.3	1.6	1.56489
AA875050	O54783	Q9Y259	AB029885	32	ESTs, Weakly similar to KICE RAT CHOLINE/ETHANOLAMINE KINASE [R.norvegicus]		1925.6	3115.6	1.6	1.61799
X65704	CAA46626	NP_003085	NM_003094	100	small nuclear ribonucleoprotein E	AA875102	3721.6	5836.1	1.6	1.56817
NM_011070	NP_035200	NP_036526	NM_012394	85	prefoldin 2 (Pfdn2),	AA891049	2802.1	4376.8	1.6	1.56197
AA891271					Mus musculus, RIKEN cDNA 2810411G23 gene		758.9	1180.5	1.6	1.55554
AA891311					EST(not recognised)		637.2	1008.9	1.6	1.58333
AF067650	AAD03414	AAD53398	AF095735	87	sarcosine dehydrogenase	AA891589	1881.1	3061.9	1.6	1.62772
AA891742					EST(not recognised)		1159.2	2836.4	1.6	2.44686
AA891828		AAH14026	BC014026	88n	Homo sapiens, Similar to RAD23		1256.5	1980	1.6	1.57581
AA891911	Q63532	g685073	S73288	61	Small proline-rich protein gene		1311.2	2124.7	1.6	1.62042
AF175224	AAG09182	AAG35611	AF202092	91	preconditioning-inducible gene 1 protein	AA892551	1170.6	1856.1	1.6	1.5856
AA892554		XP_032936	XM_032936	86n	Homo sapiens Ras-GTPase activating protein SH3 domain-binding protein 2 (KIAA0660)		1108.6	1814.9	1.6	1.63711
NM_013166	NP_037298	NP_000605	NM_000614	84	Ciliary neurotropic factor (Cntf),	AA892559	3710.9	5890.1	1.6	1.58724
AA892642					Homo sapiens mRNA; cDNA DKFZp434M229		394.3	1029.6	1.6	2.61121
AA892780					EST (not recognized)		2425.7	3841.4	1.6	1.58383
AA892805					Mus musculus adult male testis cDNA, RIKEN		1543.6	3008.2	1.6	1.94882
AA892895	R3RT15	R3HU15	J02984	100	Ribosomal protein S15		1790.6	2813.3	1.6	1.57115
AA893598	AK016067	AAH03542	BC003542	93(mus)	Mouse RIKEN full-length cDNA		696.4	1106.8	1.6	1.58932
AA893743					EST(not recognised)		1585.5	2482.1	1.6	1.5655
L18891	AAA41637	XP_048126	XM_048126	62	intracellular calcium-binding protein	AA957003	4329.2	6984.5	1.6	1.61335
AB015184	BAA32443	XP_035439	XM_035439	71	50 kD glycoprotein (Rh50)		465.7	733	1.6	1.57397
AB015637	BAA31130	NP_000139	NM_000148	76	alpha(1,2) fucosyltransferase		3790.8	6089.7	1.6	1.60644
AB017596	BAA33393	AAF36094	AF110304	73	PC1 mRNA for plasma cell membrane glycoprotein, partial cds		754.3	1188.1	1.6	1.5751
AB019393	BAA34199	NP_000252	NM_000261	78	myocilin		9560.4	13879.5	1.6	1.45177
AF019043	Q08877	JC5695	AB006965	100	Rattus norvegicus dynamin-like protein DLP1 isoform DLP1-37 mRNA, complete cds		951.1	1483.8	1.6	1.56009

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

AF031657	AAC53578	NP_003416	NM_003425	86	Zinc-finger protein 94 (Zfp94) gene, partial cds		1123.7	1795.3	1.6	1.59767
AF039085	g2773084	g2959872	AJ002308	87	Synaptogyrin 2		2137.3	3427.5	1.6	1.60366
AF041066	AAC23487	NP_002928	NM_002937	73	ribonuclease 4		477.7	749.5	1.6	1.56898
AF056324	AAC29479	NP_002958	NM_002967	74	scaffold attachment factor B; SAF-B		1237.4	2010.3	1.6	1.62462
AF065387	O88496	P38435	M81592	88	Gamma-glutamyl carboxylase		762.7	1721.4	1.6	2.25698
AF072411	AAC24876	XP_034144	XM_034144	84	fatty acid translocase/CD36 mRNA		767.6	1266	1.6	1.6493
AF072935	AAC26004	XP_053461	XM_053461	97	small GTP-binding protein rab5		1760.7	2820.7	1.6	1.60203
AF091573	AAC64594	NP_003544	NM_003553	66	HGL-SL2 olfactory receptor	AF091574	554.7	890	1.6	1.60447
AF091577	AAC64597	NP_036492	NM_012360	67	HAF-TP1 olfactory receptor		633.2	1016	1.6	1.60455
AF095741	AAC64190	XP_054663	XM_054663	66	MG87		210.5	1578.2	1.6	7.49739
AI008888	UDRTS	P04080	U46692	78	Cystatin beta		1183	1927.9	1.6	1.62987
AF361476	AAK30621	XP_053763	XM_053763	74	transcription factor MRG1	AI014091	438.5	707.9	1.6	1.61437
Y17322					CDK103	AI014135	6202.9	9862.3	1.6	1.58995
AI071511	T41751	P55196	AB011399	91	Afadin (31 on d.s.)		1213.9	1964.3	1.6	1.61817
NM_024155	NP_077069	NP_001144	NM_001153	89	ZAP 36/annexin IV (Anxa4),	AI171167	1114.3	1745.4	1.6	1.56636
U95162	AAB54065	AAH02873	BC002873	73	nuclear protein E3-3 orf3	AI171562	962.2	1559.7	1.6	1.62097
NM_031137	NP_112399	AAA63263	M55169	89	tripeptidylpeptidase II	AI178007	584.2	932.1	1.6	1.59552
NM_031797	NP_113985	NP_002222	NM_002231	62	kangai 1 (suppression of tumorigenicity 6), prostate (Kai1),	AI231213	2306.1	3804.3	1.6	1.64967
NM_017073	NP_058769	NP_002056	NM_002065	91	Glutamine synthetase (glutamate-ammonia ligase)	AI232783	10667.7	16912.8	1.6	1.58542
NM_017148	NP_058844	NP_004069	NM_004078	79	cysteine rich protein (Csrp1),	AI234146	5874	9141.7	1.6	1.5583
AI235707	P35565	P27824	L10284	84	ESTs, Highly similar to CALX RAT CALNEXIN PRECURSOR [R.norvegicus]		3286.9	5836.6	1.6	1.77572
X16979	CAA34850		No Human		MHC class I RT1.C/E (transmembrane protein)	AI235890	141.9	517.1	1.6	3.64412
AF026504	AAB81526	AAC83179	AC004974	81	SPA-1 like protein p1294	AI237576	1067.3	2250.3	1.6	2.1084
AI638985					EST(not recognised)		647.8	1434.8	1.6	2.21488
AI638980					EST(not recognised)		1376	2187.1	1.6	1.58946
AI639132					EST(not recognised)		554.2	610.2	1.6	1.10105
AI639264					EST (not recognized)		569.7	897.6	1.6	1.57557
NM_016926	NP_058622	BAA78384	AB020880	77	squamous cell carcinoma antigen recognized by T-cells 3 (Sart3),	AI639476	353.5	580.8	1.6	1.643
AI639486					EST(not recognised)		176.9	616.2	1.6	3.48332
AJ006855	S68448	O43426	AF009040	87	Synaptojanin 1		2264.6	2102.3	1.6	0.92833

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

D12573	P32076	P41211	D16593	98	Hippocalcin		1176.2	3289.6	1.6	2.7968
D14839	BAA03573	NP_002001	NM_002010	99	Fibroblast growth factor 9		2759.8	5440.1	1.6	1.97119
D31873	I58353	JP0078	D26309	95	LIM-domain containing, protein kinase		4057.2	4465.4	1.6	1.10081
D38261	BAA07413	AAG39636	AF086924	96	B-regulatory subunit of protein phosphatase 2A		3038.2	4102.1	1.6	1.35017
D84045	BAA18932	XP_043865	XM_043865	87	phosphatidylinositol 3-kinase p85 alpha subunit		545.4	846	1.6	1.55116
NM_012641	NP_036773	AAD51330	AF172331	69	regeneration protein, lithostatin, pancreatic stone protein	E01983	846.1	1320.6	1.6	1.56081
D14424	BAA03317	NP_003730	NM_003739	70	20-alpha-hydroxysteroid dehydrogenase	E06822	1026.6	1888	1.6	1.83908
H31323					Rattus norvegicus clone RP31-153J8 strain Brown Norway		832.1	1595.6	1.6	1.91756
H33219		XP_002656	XM_002656	91n	Hypothetical protein FLJ20080 (Human)		693.8	1083.3	1.6	1.5814
H33467					EST(not recognised)		496.7	812.5	1.6	1.6358
H33651					EST(not recognised)		653.2	1018.9	1.6	1.55986
J02675	AAA42113		No Human		spermine-binding protein precursor		327.9	518.1	1.6	1.58005
K03486	AAA41865	NP_002729	NM_002738	99	protein kinase C type III		191.5	833.5	1.6	4.35248
L03201	Q02765	A42482	M90696	76	Cathepsin S		1689.8	2756.4	1.6	1.6312
L23148	P41135	JC5396	U57645	90	Inhibitor of DNA binding 1, helix-loop-helix protein (splice variation)		1216	1909.7	1.6	1.57048
L35558	AAB51161	NP_004161	NM_004170	82	neuronal glutamate/aspartate transport protein		521.9	837	1.6	1.60376
M12156	AAA41314	XP_015755	XM_015755	99	helix-destabilizing protein		2251.1	3566.7	1.6	1.58443
M18331	AAA41872	NP_005391	NM_005400	98	Protein kinase C epsilon subspecies		1213	1885.2	1.6	1.55416
M33648	AAA41336	NP_005509	NM_005518	88	3-hydroxy-3-methylglutaryl-CoA synthase		2680.7	4750.7	1.6	1.77219
M34176	P21851	P21851	M34175	100	R.norvegicus beta-chain clathrin associated protein complex AP-2 mRNA, complete cds		3118.9	4895	1.6	1.56946
M36074	AAA41583	NP_000892	NM_000901	77	mineralocorticoid receptor		546.4	879.1	1.6	1.60889
M64755	AAC42063	XP_029712	XM_029712	87	cysteine sulfinic acid decarboxylase		493	770.6	1.6	1.56308
M65251	Q00900	P31629	M60119	88	Human immunodeficiency virus type I enhancer-binding protein 2		508	963.2	1.6	1.89606
M90518	AAA88788	Q14833	U92457	96	Glutamate receptor, metabotropic 4		2249.2	3509.6	1.6	1.56038
S46785	P35859	P35858	M86826	77	Insulin-like growth factor binding protein complex acid-labile subunit		888	1403.7	1.6	1.58074

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

S61948	AAB26775	NP_002465	NM_002474	97	smooth muscle myosin heavy chain isoform SM1A; SMHC SM1A		483.8	756.3	1.6	1.56325
M22063	AAA41297	XP_046330	XM_046330	91	glucose transporter protein	S68135	2074.4	3360.4	1.6	1.61994
S70804					clone p6.1 transcript		747.8	1161	1.6	1.55255
NM_012728	NP_036860	AAC50050	U01156	88	pancreatic beta cell receptor for the gluco-incretin hormone glucagon-like peptide 1	S75952	583.5	936.2	1.6	1.60446
S78556	AAB34982	NP_004125	NM_004134	93	75 kda glucose regulated protein		1317.2	2058.5	1.6	1.56278
S78744	AAC60704	AAA60181	Y00892	80	protein S=activated protein C cofactor		443.3	707.6	1.6	1.59621
NM_017044	NP_058740	NP_000306	NM_000315	71	Parathyroid hormone (Pth)	S80127	747.5	1187.9	1.6	1.58916
U12268	AAA50832	NP_001730	NM_001739	70	carbonic anhydrase V		20	1098.1	1.6	54.905
U17261	AAA56772	AAB62398	U60835	82	arylamine N-acetyltransferase-2.		360	559.2	1.6	1.55333
U32314	P52873	G01933	XM_035184	96	Pyruvate carboxylase		487.3	773.9	1.6	1.58814
U39320	AAA81372	CAC15495	AL118506	87	cysteine string protein		1441.2	2303.5	1.6	1.59832
U48592	AAB03502	NP_002173	NM_002182	86	interleukin-1 receptor accessory protein		1118.3	3018.9	1.6	2.69954
U52530	AAC53050	AAA35790	M29366	70	erbB3 proto-oncogene		1526.6	3446.3	1.6	2.2575
U56839	AAC00048	NP_002555	NM_002564	77	P2u receptor protein		1141.9	1779.4	1.6	1.55828
U57500	AAB02230	NP_002827	NM_002836	98	protein tyrosine phosphatase alpha		2527.7	4004.6	1.6	1.58429
U70268					mud-7		10364.7	19225.8	1.6	1.85493
U72350	AAB17353	XP_046220	XM_046220	91	Rattus norvegicus Bcl-xalpha mRNA, complete cds		1204.7	1973.7	1.6	1.63833
U75395	AAC52634	NP_005063	NM_005072	87	furosemide-sensitive K-Cl cotransporter		839.6	1372.2	1.6	1.63435
U76206	O35881	Q15391	D13626	80	Rattus norvegicus VTR 15-20 receptor mRNA, complete cds		469.9	739.6	1.6	1.57395
U76997	AAB19066	NP_005566	NM_005575	83	insulin-regulated membrane aminopeptidase IRAP		1658.2	2707.5	1.6	1.63279
U92564	AAB58646	BAA34480	AB018303	96	Rattus norvegicus Olf-1/EBF associated Zn finger protein Roaz mRNA, alternatively spliced form, complete cds		736.6	1179.8	1.6	1.60168
X04139	CAA27756	NP_002729	NM_002738	100	protein kinase C C-terminal region		2570	3987.5	1.6	1.55156
X14848					Rattus norvegicus mitochondrial genome	AA945152	1804.9	3397.2	1.6	1.88221
X17607	CAA35609	XP_004030	XM_004030	87	Rat beta-2 adrenergic receptor		656.6	1490.2	1.6	2.26957
X55246	CAA38987	XP_032738	XM_032738	85	inhibitory glycine receptor alpha-1 subunit		1194	1122.1	1.6	0.93978

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

X56729	CAA40053	BAA03747	D16217	56	calpastatin/CANP inhibitor		1622.2	2624.3	1.6	1.61774
X66140	CAA46930	AAG43987	AF215824	63	Epididymal apical protein I		1222.1	1428.3	1.6	1.16873
X69903	CAA49528	NP_000409	NM_000418	46	interleukin 4 receptor		3409.4	2972.9	1.6	0.87197
X80130	CAA56429	NP_005150	NM_005159	100	Alpha-actin cardiac protein		1866.1	3026.5	1.6	1.62183
X97443	CAA06212	P49755	X97442	96	Integral membrane protein Tmp21-I (p23)		1836.7	2913.7	1.6	1.58638
Y13381	CAA73808	NP_001626	NM_001635	70	Amphiphysin		1054.7	1679.3	1.6	1.59221
Z17319	CAA78967	P15259	J05073	93	Phosphoglyceromutase		1976.1	3134.9	1.6	1.58641
Z29072	CAA82313	AAB95295	L21998	63	Mucin		626.4	839.1	1.6	1.33956
NM_031577	NP_113765	NP_066567	NM_021081	55	growth hormone releasing hormone	Z34004	675	1619.9	1.6	2.39985
NM_012520	NP_036652	NP_001743	NM_001752	88	Catalase	AA926149	1104.4	1805.6	1.6	1.63491
X80130	CAA56429	NP_005150	NM_005159	100	alpha-actin cardiac	AI104567	298.7	775.7	1.6	2.59692
U17837	AAA74468	NP_036363	NM_012231	67	zinc finger protein RIZ		1624.6	1443.6	1.6	0.88859
X78848	CAA55405	NP_000838	NM_000847	75	glutathione S-transferase Yc1 subunit	S72505	2031.5	1905.5	1.6	0.93798
AA684919					EST (not recognized)		2838.5	4290.8	1.5	1.51164
AA686164					Mus musculus, Similar to dendritic cell protein, clone MGC:11741		400.4	614.9	1.5	1.53571
AA799497					Mus musculus 18 days embryo cDNA, RIKEN		889.4	1375.3	1.5	1.54632
AA799511		AAC09039	AC004520	97	Homo sapiens BAC clone CTB-119C2 from 7p15, complete sequence (similar to NFE2-related transcription factors)		699.5	1062.2	1.5	1.51851
AA799518					EST(not recognised)		998.7	1074	1.5	1.07756
NM_028162	NP_082428	XP_050855	XM_050855	82	MMS19	AA799566	12231.9	17792.2	1.5	1.45457
X51705	CAA36001	NP_009140	NM_007209	71	ribosomal protein L35.	AA799571	5040.4	9241.4	1.5	1.83347
NM_031331	NP_112621	NP_002801	NM_002810	88	proteasome (prosome, macropain) 26S	AA799887	7597.9	11060.1	1.5	1.45568
AA799891					Mus musculus adult male hippocampus cDNA, RIKEN		487.1	732.3	1.5	1.50339
AA800170		NP_003434	NM_003443	38	ESTs, Weakly similar to ECTODERM-NEURAL CORTEX-1 PROTEIN (ENC-1) [M.musculus]		2268.2	2340.6	1.5	1.03192
AA800177					EST (not recognized)		1197.3	1747	1.5	1.45912
AA800212	A30594	P16614	M23115	98	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2		3066.9	3515.5	1.5	1.14627
AF364071	AAK50399	NP_055147	NM_014332	81	SMPX protein	AA800221	779.8	1146.9	1.5	1.47076

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

AA800260					EST (not recognized)		420.3	631.3	1.5	1.50202
NM_020584	NP_065589	XP_049964	XM_049964	41	sulfotransferase-related protein SULT-X1	AA800315	804.7	1207.7	1.5	1.50081
AA800613	P47973	S34427	M63625	86	Rattus norvegicus gene for TIS11		1596.4	1734.4	1.5	1.08644
AA800881					EST(not recognised)		3330.4	7821.1	1.5	2.3484
AF016049	AAC27975	NP_000421	NM_000430	99	platelet-activating factor acetylhydrolase beta subunit (PAF-AH beta)	AA801441	3260.6	4848.1	1.5	1.48687
M31363	AAA41356	NP_003158	NM_003167	60	hydroxysteroid sulfotransferase	AA817987	1092.4	909.7	1.5	0.83275
NM_012925	NP_037057	NP_000602	NM_000611	49	CD59 antigen	AA818025	23194.7	34177.6	1.5	1.47351
AA859585					Mus musculus adult male cerebellum cDNA, RIKEN		1455.3	2772.8	1.5	1.90531
AA859909					EST(not recognised)		868.3	1331.8	1.5	1.5338
AA860044	AAH03203	CAB45016	Z93930	87n	Contains the XBP1 gene for X-box binding protein 1		1528.4	2272.5	1.5	1.48685
NM_017158	NP_058854	NP_000760	NM_000769	72	cytochrome P450, 2c39	AA866240	2650.2	4008.7	1.5	1.5126
AA866409		XP_031553	XM_031553	84	Homo sapiens KIAA0332 protein (KIAA0332)		1182.9	1831.8	1.5	1.54857
AA866439					EST(not recognised)		3555.1	5343.2	1.5	1.50297
AA874857					Homo sapiens PAC clone RP4-673M15		366.8	533.8	1.5	1.45529
AA875194					EST(not recognised)		1240.3	2073.8	1.5	1.67201
AA875500		XP_047123	XM_047123	87n	Homo sapiens KIAA1460 protein		876.4	1066.6	1.5	1.21702
NM_009745	NP_033875	NP_001698	NM_001707	74	B-cell CLL/lymphoma 7B (Bcl7b),	AA875661	1447.4	2112.7	1.5	1.45965
NM_009274	NP_033300	XP_004842	XM_004842	80	serine/arginine-rich protein specific kinase 2	AA891069	964.5	1409.9	1.5	1.46179
AF253473	AAK29279	NP_061967	NM_019094	85	diphosphoinositol polyphosphate phosphohydolase type II	AA891107	949.1	2512.9	1.5	2.64767
NM_031026	NP_112288	NP_006132	NM_006141	90	LIC-2 dynein light intermediate chain 53/55	AA891132	699.5	1268.6	1.5	1.81358
AA891700					EST (moderately similar to human transmembrane protein)		563.1	818.7	1.5	1.45392
AA891738	Q07116	P51687	L31573	87	Sulfite oxidase		1424.6	2154	1.5	1.512
AA891800					Mus musculus 18 days embryo cDNA, RIKEN		1160.6	1773.5	1.5	1.52809
AA891922			AC021396	86n	Homo sapiens, clone RP11-281I2, complete sequence		506.7	591.3	1.5	1.16698
AA891998					EST(not recognised)		1404.6	2138.1	1.5	1.52221

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

AA892248					Rattus norvegicus mitochondrial genome		80657	120243.3	1.5	1.4908
AA892300		XP_043322	XM_043322	92n	peroxisome receptor 1 (PXR1)		1003.7	1472.2	1.5	1.46677
AA892313					Mus musculus 10 days embryo cDNA, RIKEN		2396.2	3538	1.5	1.4765
NM_022298	NP_071634	XP_028662	XM_028662	93	alpha-tubulin	AA892333	19107	29544.5	1.5	1.54627
AA892507	BAB22691	Q14197	X81788		ESTs, Moderately similar to DS1_HUMAN DS-1 PROTEI					
				83n	[H.sapiens]		1080.7	1320.9	1.5	1.22226
AA892531	B39066	PIHUB6								
				38	ESTs, Weakly similar to B39066 proline-rich protein 15 - rat [R.norvegicus]		3310.7	4963.6	1.5	1.49926
AA892557					Mus musculus 18 days embryo cDNA, RIKEN		1159.2	1694.8	1.5	1.46204
Z34922	CAA84402	NP_001354	NM_001363	81	nucleolar protein NAP57	AA892562	2437.1	3631.9	1.5	1.49025
AA892753					Mus musculus adult male testis cDNA, RIKEN		2690.2	4157.8	1.5	1.54554
AA892851		AAC50062	U02680		EST, weakly similar to Human protein					
				93n	tyrosine kinase		290.2	770.6	1.5	2.65541
AA892921					Mus musculus RIKEN cDNA 2210417O06		2594.7	3894.4	1.5	1.50091
AA892986					Mus musculus, Similar to glycogenin 2, clone MGC:6424 IMAGE:3593927		1147.6	1673.5	1.5	1.45826
AA893011					Mus musculus, Similar to cytochrome P450, 4a10, clone MGC:25972		1674.6	2580.7	1.5	1.54108
NM_018737	NP_061207	NP_062831	NM_019857		cytidine 5'-triphosphate synthase 2; CTP					
				83	synthetase homolog	AA893059	1177.9	1725.1	1.5	1.46456
NM_023721	NP_076210	NP_057078	NM_015994		ATPase, H+ transporting lysosomal vacuolar proton pump); V-ATPase					
				92	subunit D	AA893246	4082.1	5935.6	1.5	1.46121
AF285154					solute carrier family 10 member 2 gene	AA893260	3608.1	5319	1.5	1.47418
NM_013731	NP_038759	XP_009494	XM_009494							
				90	serum/glucocorticoid regulated kinase 2	AA893436	3602.5	5227.2	1.5	1.45099
U51017	AAB39509	NP_006206	NM_006215	53	kallistatin	AA893552	898	1335	1.5	1.48664
AA893607					Mus musculus, Similar to paxillin, clone IMAGE:3583842		1186.3	1973.4	1.5	1.66349
AA893670					EST (not recognized)		2199.9	3208.3	1.5	1.45838

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

AA893671	Q63244	1923399A	U02310							
AF275151	AAF86977	XP_039385	XM_039385	93	ESTs, Weakly similar to HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 1 [R.norvegicus]		868.4	1329.2	1.5	1.53083
AA893994				73	androgen receptor-related apoptosis-associated protein CBL27	AA893853	2538.8	2873.8	1.5	1.13195
NM_032083	NP_114472	CAA35769	X51408	97	Mus Musculus Strain C57BL6/J Chromosome 11 Clone RP23-271O13 chimerin (chimaerin) 1 (Chn1),	AA894317	1119.7 4075.2	1677.7 6194.9	1.5 1.5	1.49835 1.52015
AB006446										
NM_007377	NP_031403	NP_004911	NM_004920	85n	topoisomerase II alpha, 3' untranslated	AA899854	784.1	1174.4	1.5	1.49777
AA926242	S22415	g1518269	X94333	56	apoptosis-associated tyrosine kinase (Aatk)	AA925717	5919.7	8835.6	1.5	1.49258
AF302085	AAG21394	NP_001736	NM_001745	50	Trans-Golgi network integral membrane protein TGN38		544	789.8	1.5	1.45184
AA956941	Q62655	P15884	M74719	81	calcium-modulating cyclophilin ligand	AA943387	1764.8	2579.1	1.5	1.46141
X78604	CAA55338	AAD40383	AF100740	97	R8f DNA-binding protein		766.9	1166.7	1.5	1.52132
AB002169				99	ARF-like protein 5	AA956958	413	610.5	1.5	1.47821
AB004277	BAA20360	NP_061752	NM_018929	72	RT1.P1 pseudogene for TL antigen Protocadherin 5		3944.2	5792.3	1.5	1.46858
AB009889	BAA32480	NP_000939	NM_000948	26	prolactin-like protein H		5498.4	8112.3	1.5	1.47539
AB011528	BAA32459	XP_042739	XM_042739	63	MEGF2		468.8	687.2	1.5	1.46587
AB011544	BAA32734	NP_003311	NM_003320	77	TUBBY protein		1032.6	2592.9	1.5	2.51104
AB017140	BAA34311	NP_004263	NM_004272	91	PSD-Zip45		816.7	1193.8	1.5	1.46174
AB017188	BAA32596	NP_002801	NM_002810	88	antisecretory factor		1317.3	1708.7	1.5	1.29712
AF000899	AAC82319	XP_037529	XM_037529	83n	p58/p45 mRNA, alternatively spliced form		13322.7	19353.8	1.5	1.45269
AF000942	P41138	Q02535	X69111	96	Inhibitor of DNA binding 3, dominant negative helix-loop-helix protein		504.6	775.8	1.5	1.53746
AF000973	AAB82740	XP_012875	XM_012875	75	Calcium-activated potassium channel (rSK1) mRNA		1549.1	1793.7	1.5	1.1579
AF007107	AAB67609	AAA63169	L39945	89	cytochrome b5		1228.2	2938.9	1.5	2.39285
AF009604	O35180	Q99963	X99664	86	SH3 domain protein 2 C1		2764.6	4672.9	1.5	1.69026
AF029107	AAC05305	NP_005494	NM_005503	82	Mint2; neuronal munc18-1 binding protein		1335.1	743.8	1.5	0.55711
AF030358	AAC33834	AAB49879	U84487	63	Rattus norvegicus chemokine CX3C mRNA, complete cds		1465.4	1877.6	1.5	1.28129
AF031528	AAB86946	NP_064445	NM_020061	89	green-sensitive opsin		1228.3 2295.2	3071.3 4145.2	1.5 1.5	2.50045 1.80603

able 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

AF032666	AAC01578	CAB54145	AL031770		Rattus norvegicus rsec5 mRNA, complete cds		1759.7	2558	1.5	1.45366
AF032872	AAC40114	XP_055306	XM_055306	94	potassium channel regulatory protein KChAP		1556.3	2352.4	1.5	1.51153
AF036761	AAB88865	AAD29870	AF097514	88	stearoyl-CoA desaturase 2		6600.8	9764.2	1.5	1.47924
AF039218	T14039	O14578	AC002563	92	Postsynaptic density protein (citron)		1081.9	1611.2	1.5	1.48923
AF039584	AAC77439	XP_052060	XM_052060	96	Decay accelerating factor soluble-form precursor (DAF) mRNA, complete cds		2114.9	1938.2	1.5	0.91645
AF040261	AAC98929	XP_008271	XM_008271	47	Phosphatidylcholine transfer protein (Pctp)		781.8	1193.4	1.5	1.52648
AF069775	AAC21580	AAB60937	AF002246	81	Rattus norvegicus L1-like cell adhension molecule (CALL) mRNA		422.9	686	1.5	1.62213
AF079162	AAC99398	NP_000255	NM_000264	90	Rattus norvegicus patched (ptc) mRNA, partial cds		3093.1	7339.6	1.5	2.37289
AF081365	2009199A	C55119	U03884	92	Potassium inwardly-rectifying channel, subfamily J		882.2	1973.1	1.5	2.23657
AF083330	AAC33291	XP_039750	XM_039750	95	kinesin-like protein KIF3C		2301.6	3216.4	1.5	1.39746
AF087037	AAC34894	XP_012976	XM_012976	82	BTG3		523.3	983.6	1.5	1.87961
AF089839	AAC83035	XP_032173	XM_032173	83	N-ethylmaleimide sensitive factor		608	889.4	1.5	1.46283
AF091247	AAC79846	NP_004510	NM_004519	96	Rattus norvegicus potassium channel (KCNQ3)		2853.5	4894.7	1.5	1.71533
AF091578	AAC64598	NP_006628	NM_006637	95	Rattus norvegicus isolate EVA-TN1 olfactory receptor mRNA, partial cds		1504.5	2328.9	1.5	1.54796
AF110508	AAC95393	NP_000594	NM_000603	47	endothelial nitric oxide synthase		1200.6	1820	1.5	1.51591
AI008852	g1220484	P04720	X03558	97	Eukaryotic translation elongation factor 1 alpha 2		5992.4	10085	1.5	1.68297
NM_012588	NP_036720	XP_038125	XM_038125	99	insulin-like growth factor-binding protein (IGF-BP3)	AI009405	393	601.9	1.5	1.53155
AI010371				76	EST(not recognised)		853.9	805.4	1.5	0.9432
NM_012699	NP_036831	NP_036460	NM_012328		microvascular endothelial differentiation gene 1	AI011998	628.1	964.2	1.5	1.53511
Y07783	CAA69106	NP_003704	NM_003713	86	ER transmembrane protein	AI013472	2233.3	3375.7	1.5	1.51153
AI029805	1CKTA	S02826	X12597	91	High mobility group 1		325.5	503.9	1.5	1.54808
U35245	AAC52986	BAB55345	AK027754	99	vacuolar protein sorting homolog r-vps33b	AI059863	3212.3	4657.9	1.5	1.45002
M25888	AAA41888	NP_000524	NM_000533	96	ilpophilin	AI072770	2534.4	3793.1	1.5	1.49665
AI072943	P47971	Q15818	U61849	100	Rattus norvegicus neuronal pentraxin precursor mRNA, complete cds		2119.6	3278.5	1.5	1.54675
				95						

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

AI073164					EST(not recognised)		1209.2	2412	1.5	1.99471
U70050	AAC52946	NP_002217	NM_002226	82	jagged2 precursor	AI101320	3368.2	2614	1.5	0.77608
M15883	AAA40890	NP_009028	NM_007097	90	clathrin light chain (LCB2)	AI102411	660.8	823.6	1.5	1.24637
AF259874	AAK69389	XP_027464	XM_027464	90	phosphoserine aminotransferase	AI102868	967.6	1202.1	1.5	1.24235
AI104679					Mus musculus adult male kidney cDNA, RIKEN		6471.6	9541.9	1.5	1.47443
NM_013030	NP_037162	AAH11351	BC011351	83	solute carrier family 17 (sodium/hydrogen exchanger)	AI105198	1615.8	3846.6	1.5	2.38062
M96374	AAA41704	AAF03536	AC007462	97	neurexin I-alpha.	AI146018	2301	3517.7	1.5	1.52877
NM_031552	NP_113740	NP_058432	NM_016824	86	Adducin 3, gamma	AI146195	2549.9	3812	1.5	1.49496
M94040	AAA73899	NP_000047	NM_000056	83	branched chain alpha-keto acid dehydrogenase E1-beta subunit	AI168942	1473.4	2616.3	1.5	1.77569
Z11663	CAA77731		no human		CD24	AI171462	4434.8	6452.1	1.5	1.45488
NM_031020	NP_112282	CAB08440	Z95152	94	p38 mitogen activated protein kinase	AI171630	1355.7	3214.5	1.5	2.3711
NM_012904	NP_037036	NP_000691	NM_000700	89	annexin 1 (p35) (Lipocortin 1)	AI171962	2194.2	3362.8	1.5	1.53259
M86389	AAA41353	NP_001531	NM_001540	82	heat shock protein 27 (Hsp27)	AI176658	28481.7	47185.4	1.5	1.65669
AI177161	O54968	I59340	S74017	82	NF-E2-related factor 2		1054.2	1551	1.5	1.47126
AI179916					Mus musculus brain cDNA, clone MNCb 1308		2293.5	3537.4	1.5	1.54236
AI180442	A34713	P14324	J05262	85	Testis-specific farnesyl pyrophosphate synthetase		2220.3	3260.9	1.5	1.46868
D87671	BAA13432	NP_060918	NM_018448	94	TIP120	AI230395	1545.2	2326.9	1.5	1.50589
NM_019123	NP_061996	CAC07404	AJ271734	54	sialyltransferase 7 ((alpha-N-acetylneuraminyl 2,3-betagalactosyl-1,3) N-acetyl galactosaminide alpha-2,6-sialyltransferase) C	AI231519	732.9	1081.1	1.5	1.4751
AI232012	BAB22322	XP_005415	XM_005415	83n	Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8		6804.7	12266.8	1.5	1.8027
D85189	BAA22185	CAA73314	Y12777	95	Acyl-CoA synthetase	AI236284	944.8	2775.4	1.5	2.93755
X64411	CAA45756	NP_056988	NM_015902	83	100 kDa protein	AI237592	2001.5	2174.1	1.5	1.08624
AI639001					EST (not recognized)		558.6	1318.5	1.5	2.36037
AI639019					EST(not recognised)		447.1	522.6	1.5	1.16887
AI639074					EST(not recognised)		999.9	2725.9	1.5	2.72617
AI639141					Mus musculus 11 BAC RP23-362J7		758.4	1116.7	1.5	1.47244
AI639255					EST(not recognised)		1920.9	2845.7	1.5	1.48144
AI639364					EST(not recognised)		914.9	1767.3	1.5	1.93169
AI639391					EST (not recognized)		4424.1	6525.4	1.5	1.47497
AI639427					EST (not recognized)		1097.8	1634	1.5	1.48843

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

AI639432 AI639447					EST (not recognized)		1428	2207.8	1.5	1.54608
NM_031669	NP_113857	AAL16670	AF421885		Mus musculus 18 days embryo cDNA, RIKEN uterine-specific proline-rich acidic protein		703.9	1363.7	1.5	1.93735
				52		AI639531	781.5	1181.9	1.5	1.51235
AJ001320	CAA04681	NP_003820	NM_003829	77	Multiple PDZ domain protein		743.7	1458.7	1.5	1.98141
AJ006084	CAA06836	NP_055140	NM_014325	73	coronin-like protein		2311.7	1603.2	1.5	0.69352
AJ010386	CAA09103	XP_043098	XM_043098	78	ETR-R3b protein		528.7	813.6	1.5	1.53887
D00512	BAA00401	NP_000010	NM_000019	76	mitochondrial acetoacetyl-CoA thiolase		672.6	996.7	1.5	1.48186
D10754	BAA01586	XP_027825	XM_027825	84	proteasome subunit R-DELTA		4768.6	7943.6	1.5	1.66581
D12927	BAA02310	NP_003186	NM_003195	85	transcription elongation factor S-II		1165.3	1720.9	1.5	1.47679
D17614	BAA04533	NP_006817	NM_006826	99	14-3-3 protein theta-subtype		4050.8	5024.3	1.5	1.24032
D26500	BAA05508	NP_001363	NM_001372	80	Dynein-like protein 9A, partial cds		831	1285.8	1.5	1.54729
D31873	I58353	JP0078	D26309	95	LIM-domain containing, protein kinase		1533.4	2242.2	1.5	1.46224
D37880	P55146	A53743	L24529	89	Bruton agammaglobulinemia tyrosine kinase (32 on d.s.)		1280.7	1910.1	1.5	1.49145
D38072	BAA07266	XP_056374	XM_056374	97	protein tyrosine phosphatase		800.6	1163.9	1.5	1.45378
D49434	BAA08412	AAA51784	J05225	80	Arylsulfatase B		356.9	530.8	1.5	1.48725
U32170	AAD03478	NP_004674	NM_004683	74	senescence marker protein-30 (SMP30) gene (regucalcin)	D67071	881.8	1279.2	1.5	1.45067
D83661	BAA12035	AAB60366	U20141	79	inducible nitric oxide synthase		606.3	937.9	1.5	1.54692
D85844	BAA21782	XP_008531	XM_008531	93	rabaptin-5		2591.5	3853.6	1.5	1.48702
D90404	A41158	S66504	X87212	78	Cathepsin C (dipeptidyl peptidase I)		461.7	670.9	1.5	1.45311
H31217					EST (not recognized)		985.6	1497.7	1.5	1.51958
NM_013625	NP_038653	NP_000421	NM_000430	99	platelet-activating factor acetylhydrolase	H31367	12809.7	19539.5	1.5	1.52537
H31479		AAF69029	AF132811	88n	Nectin-like protein 2		5831.4	8945.5	1.5	1.53402
H31590					EST(not recognised)		381.4	733.5	1.5	1.92318
H33149					Mus musculus, Similar to hypothetical protein FLJ11200, clone MGC:7482		456.2	921.7	1.5	2.02039
H33528					Homo sapiens chromosome 17, clone hRPK.214_C_8		1554.6	2358.7	1.5	1.51724
J01435					Rattus norvegicus mitochondrial genome		67882.6	102306	1.5	1.5071
J02649	AAA66036	XP_009351	XM_009351	93	H+,K+-ATPase		1398.5	2050	1.5	1.46586
J04503	AAA41917	NP_066283	NM_021003	98	protein phosphatase 2c.		1337.9	1947.8	1.5	1.45586
L00191	AAA41166	AAA52462	M10905	76	fibronectin 1		3431.7	5347.1	1.5	1.55815

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

L01702	AAA41983	CAA37447	X53364	89	Tryosine-phosphatase (LRP)		831.9	1690.1	1.5	2.03161
L04485	AAA41571	NP_002746	NM_002755	90	MAP kinase kinase		5954.3	8837.6	1.5	1.48424
L05489	Q06175	Q99075	M60278	81	Diphtheria toxin receptor (heparin binding epidermal growth factor - like growth factor)		417.5	606.4	1.5	1.45246
L10072	AAA40615	NP_076917	NM_024012	81	serotonin receptor		957.1	1466.8	1.5	1.53255
L10362	S34961	g3882191	AB018278	94	Rattus norvegicus synaptic vesicle protein 2B (SV2B) mRNA, complete cds		1122.8	1675.3	1.5	1.49207
L10669	AAA41253	XP_050619	XM_050619	79	glycogen phosphorylase		2267.9	3493.5	1.5	1.54041
L10669	AAA41253	XP_050619	XM_050619	79	glycogen phosphorylase		810.4	1190.5	1.5	1.46903
L13619	A47112	O15503	U96876	84	Growth response protein (CL-6)		3620	5524.1	1.5	1.52599
L14684	AAA41107	NP_079272	NM_024996	82	elongation factor G.		682.4	1054.7	1.5	1.54557
L14937	AAA41816	NP_002560	NM_002569	60	proprotein convertase 4.		1199.3	1764.9	1.5	1.47161
L23219	I56580	JW0050	AB010414	94	Guanine nucleotide binding protein (G protein), gamma 7 subunit		3491.4	5178.8	1.5	1.4833
L26525	AAA21089	XP_004559	XM_004559	80	tyrosine kinase receptor (Ptk-3) gene		1533.1	2245.4	1.5	1.46461
L34074	AAC37675	NP_149046	NM_033057	84	OL1 receptor		568.9	879.8	1.5	1.54649
L34821	P51650	g3766467	g3766467	88	Succinic semialdehyde dehydrogenase		452.9	930	1.5	2.05343
M11598	P10093	P08881	X15943	72	Rat beta-type calcitonin gene-related peptide mRNA, complete cds		2741.1	4206.8	1.5	1.53464
M15883	AAA40890	NP_009028	NM_007097	90	clathryn light chain (LCB2).		3715	5568.3	1.5	1.49887
M17527	1GP2	RGHUI1	M17219	99	Guanine nucleotide binding protein, alpha inhibiting 1		957.7	1416.5	1.5	1.47906
M18416	AAA61927	NP_001955	NM_001964	72	nerve growth factor-induced protein.		1039	1560.5	1.5	1.50192
M23643	RHRTT	P20396	M63582	55	Thyrotropin releasing hormone		1425.1	2980.5	1.5	2.09143
M24104	1SFCA	P19065	AF135372	98	Vesicle-associated membrane protein (synaptobrevin 2)		8839.3	11107	1.5	1.25655
NM_012541	NP_036673	XP_044660	XM_044660	74	cytochrome P450	M26127	1082	1615.8	1.5	1.49335
M31178	KLRTB	S00234	X06661	98	Cerebellar Ca-binding protein, spot 35 protein		1341.9	2074.9	1.5	1.54624
M34238	AAA40889	NP_002496	NM_002505	55	CCAAT binding transcription factor-B subunit (CBF-B)		1331.3	2063.8	1.5	1.55021
M38566	AAB02287	NP_000775	NM_000784	70	cytochrome P450		631.7	951.6	1.5	1.50641
M64378	AAA41741	AAK95089	AF399804	70	Olfactory protein		1061.2	1620.4	1.5	1.52695
M64780	AAA40703	AAC39776	AF016903	77	agrin		2230.8	4258.7	1.5	1.90905
M64793	AAA42064		No human		Rat salivary proline-rich ı (RP15)		879.8	1341.5	1.5	1.52478

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

M80550	AAA40682	BAA83012	AB028983	94	adenylyl cyclase type II		3740.8	5662	1.5	1.51358
M83143	P13721	P15907	X17247	80	beta-galactoside-alpha 2,6-sialyltransferase		1393.7	2541.1	1.5	1.82328
M83678	P35286	P51153	X75593	90	RAB13		1474.4	3247.8	1.5	2.20279
M83679	AAA41995	XP_050525	XM_050525	52	RAB15		1187.3	1728.5	1.5	1.45582
M87786	AAA41369		No Human		Immunoglobulin light chain variable region		1503.8	2228.3	1.5	1.48178
M93669	S02180	A34174	M25756	80	Secretogranin II		3027.8	4399.5	1.5	1.45304
M94287	AAA41718	AAH01883	BC001883	42	Nopp140		3752.7	4182.7	1.5	1.11458
M99567	A45493	I38994	U26425	92	Rattus norvegicus phospholipase C beta-3 mRNA, partial cds		2124.7	3247.6	1.5	1.5285
S42358	AAB22850	NP_055044	NM_014229	90	GABA transporter; GAT-B		1545.5	2295	1.5	1.48496
S46785	P35859	P35858	M86826	77	Insulin-like growth factor binding protein complex acid-labile subunit		3015.1	4397.1	1.5	1.45836
S48190	AAB23958	NP_001607	NM_001616	90	type II activin receptor; rActR-II		619.6	1477.3	1.5	2.38428
S56508	AAB19809	XP_029111	XM_029111	92	Phosphatidylinositol 4-kinase		315.1	700.4	1.5	2.22279
S65091		XP_002992	XM_002992	87	Cyclic AMP phosphoprotein, 19kD		2091.4	3071.3	1.5	1.46854
S79213	AAB35244	NP_006232	NM_006241	80	phosphatase inhibitor-2; I-2		8774.4	13427.7	1.5	1.53033
NM_031798	NP_113986	NP_000329	NM_000338	63	solute carrier family 12, member 2	S82233	985.3	1002	1.5	1.01695
S83279	AAB49519	NP_000405	NM_000414	83	HSD IV=peroxisome proliferator-inducible gene		1744.8	2615.2	1.5	1.49885
S98336	AAB22104	XP_009274	XM_009274	62	Mullerian inhibiting substance		5066.3	4922.4	1.5	0.9716
U02320	AAA19945	NP_039251	NM_013957	90	Rattus norvegicus clone ndf40 neu differentiation factor		893.6	1361.6	1.5	1.52372
U09211	AAA20498	NP_003046	NM_003055	87	Vesicular acetylcholine transporter mRNA		3715.9	5435.8	1.5	1.46285
U10354	P48442	P41180	U20759	93	Calcium-sensing receptor (hypocalciuric hypercalcemia 1, severe neonatal hyperparathyroidism)		1040.3	1608.6	1.5	1.54628
U16245	AAA66221	NP_001642	NM_001651	77	Aquaporin-5		2799.8	4313.6	1.5	1.54068
U17254	JQ0623	P22736	D49728	91	Immediate early gene transcription factor NGFI-B		3778.6	5588.3	1.5	1.47893
U17919	AAA80105	NP_001614	NM_001623	89	allograft inflammatory factor-1.		961.5	1485.2	1.5	1.54467
U20907	AAC52233	NP_000861	NM_000870	92	5-HT4L receptor		1072.7	1165.3	1.5	1.08832
NM_019553	NP_062426	NP_004719	NM_004728	78	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 21 (RNA helicase II/Gu) (Ddx21)	U21719	613	784.6	1.5	1.27993
U26033	AAC52317	AAF03234	AF168793	82	carnitine octanoyltransfi		553.7	538	1.5	0.97165

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

U39875	AAB04146	NP_009167	NM_007236	98	EF-hand Ca2+ binding protein p22		2826.8	4133.9	1.5	1.4624
U47014	AAA87888	AAA91807	U49114	48	pro-protein convertase 5 isoform B.		2399	3538.8	1.5	1.47511
U47110	AAB19127	AAB88198	AF035582	94	peripheral plasma membrane protein CASK		383.9	584.7	1.5	1.52305
U49058	AAC52659		no human		CTD-binding SR-like protein rA4 mRNA, partial cds		1272.1	1866.9	1.5	1.46757
U50185	AAA92961	XP_028840	XM_028840	37	protein phosphatase 1	AA800549	1433.4	2123.7	1.5	1.48158
U52663	AAC05607	AAD01439	AF010472	88	peptidylglycine alpha-amidating monooxygenase (PAM) gene		2671.1	4120.2	1.5	1.54251
U57062	g1470062	g338011	J03189	59	Natural killer cell protease 4 (RNKP-4) (47 on d.s.)		371.5	540.4	1.5	1.45464
U59672	AAB18293	P46098	D49394	85	5-Hydroxytryptamine (serotonin) receptor 3A		1663	2414.8	1.5	1.45207
U61729	AAB09057	NP_006804	NM_006813	62	Rattus norvegicus proline rich protein mRNA, complete cds	AI235492	753.2	1100.2	1.5	1.4607
U66478	AAC52943	S68987	U59423	98	MAD (mothers against decapentaplegic, Drosophila) homolog 1		439.9	682.2	1.5	1.55081
U67081	AAB40718	AAF14051	AF036943	90	C2-HC type zinc finger protein r-MyT2 mRNA		2253.3	3324.5	1.5	1.47539
U67910	AAB48263	XP_018104	XM_018104	76	Mast cell protease 7 (RMCP-7)		1237.4	1802.2	1.5	1.45644
U75392	AAB18747	NP_009204	NM_007273	80	B-cell receptor associated protein 37		4147.6	5070.7	1.5	1.22256
NM_012551	NP_036683	NP_001955	NM_001964	72	Early growth response 1 (Egr1),	U75397	831.8	722.7	1.5	0.86884
U75920	AAB81885	NP_036457	NM_012325	95	APC binding protein EB1		1320.7	1941.9	1.5	1.47036
U76635	AAB71495	NP_005214	NM_005223	71	Deoxyribonuclease I (DNaseI) ??	AI639157	1989.7	3083.8	1.5	1.54988
U77626					formin binding protein 21 mRNA		538.6	581.2	1.5	1.07909
U77931	AAK21974		No Human		rRNA promoter binding protein		13221.3	17597.9	1.5	1.33103
U89529	AAC53424	XP_026964	XM_026964	58	Rattus norvegicus fatty acid transport protein mRNA, complete cds		2219.7	3371.9	1.5	1.51908
U89743	AAB49893		No human		Rattus norvegicus unknown protein		822.4	1227.9	1.5	1.49307
U89905	AAB72145	XP_043771	XM_043771	75	Methylacyl-CoA racemase alpha		1207	1763.5	1.5	1.46106
U90829	AAD09247	NP_003896	NM_003905	96	APP-binding protein 1		298.4	1348.6	1.5	4.51944
U76112	AAC53095	NP_001409	NM_001418	85	translation repressor NAT1	U95052	13013.1	18875.7	1.5	1.45052
U95178	AAC33406	AAB19032	U41111	81	DOC-2 p59 isoform		793.7	1153.6	1.5	1.45345
U95727	AAB64094	NP_005871	NM_005880	86	DnaJ (Hsp40) homolog, subfamily A, member 2		1323.9	1773.8	1.5	1.33983

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

X02601	P03957	AAA36321	J03209		53 kD polypeptide induced by growth factors (EGF) and oncogenes (H-ras;				
X07467	S01233	P11413	X03674	83n	src; polyoma middle T)		536	828	1.5	1.54478
X12535	CAA31053	XP_031588	XM_031588	93	Glucose-6-phosphate dehydrogenase		6985.4	10384.5	1.5	1.4866
X13412	CAA31778	NP_005237	NM_005246	99	Ras-related protein p23		4338	6653.7	1.5	1.53382
X13804	CAA32038	XP_037942	XM_037942	92	flk protein		609.7	708.4	1.5	1.16188
X17053	CAA34901	NP_005399	NM_005408	87	Heavy neurofilament polypeptide (854 AA)		33801.6	50718.1	1.5	1.50046
X17611	CAA35613	XP_044141	XM_044141	53	Immediate-early serum-responsive JE gene (6 on d.s.)		1204.5	2430.4	1.5	2.01777
X52840	P18666	MOHULP	X54304	77	precursor polypeptide		2213	3289.6	1.5	1.48649
X53773	CAA37791	AAD15564	AC006942	97	Myosin regulatory light chain		888.9	1331.6	1.5	1.49803
X56596	P29826	P05538	M11136	73	alpha-c large chain (AA 1-938)		660.4	1022.6	1.5	1.54848
X58631	PT0183	I78844	L36645	74	MHC class II antigen RT1.B-1 beta-chain		2144.1	3284.8	1.5	1.53202
X59677	CAA42203	NP_003975	NM_003984	94	ESTs, Highly similar to PT0183 protein-tyrosine kinase [R.norvegicus]		1818.4	1412.2	1.5	0.77662
X62325				88	Rattus sp. cDNA for M2 gene (clone M2-798)		5779.8	8769.1	1.5	1.5172
X68782	CAA48681	AAH09851	BC009851		R.rattus TcRValphaT48a2 mRNA for T cell receptor V-alpha J-alpha		2727.5	4169.2	1.5	1.52858
X78949	CAA55546	XP_032511	XM_032511	59	Ig heavy chain VDJ-region CH1-CH2		921.2	1412	1.5	1.53278
X82445	CAA57825	CAB66659	AL136725	92	Prolyl 4-hydroxylase alpha subunit		2312.4	3355.6	1.5	1.45113
Y14706	CAA75008	NP_005284	NM_005293	81	RnudC		4491.4	6577.9	1.5	1.46455
Y17048	MCRT	NP_112482	NM_031205	70	putative G-protein coupled receptor		4977.9	7491.4	1.5	1.50493
NM_008139	NP_032165	AAC50363	U40038	98	Rattus norvegicus mRNA for caldendrin		2113.6	3203.6	1.5	1.51571
Z11995	Q99068	P30533	M63959	94n	guanine nucleotide binding protein, alpha q polypeptide (Gnaq)	Y17164	1173.8	1794.2	1.5	1.52854
Z12298	CAA78170	NP_001911	NM_001920	76	ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN PRECURSOR	AA892810	1072.7	2346.4	1.5	2.18738
Z68145	CAA92268	CAC51026	AJ318022	74	dermatan sulfate proteoglycan-II (decorin)		24967.7	37602.5	1.5	1.50605
AB017188	BAA32596	NP_002801	NM_002810	62	lambda-5		2343.2	2483.4	1.5	1.05983
Y17322				88	antisecretory factor		5391.3	8075.4	1.5	1.49786
					CDK103	AI014135	275.9	642.2	1.5	2.32765

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

NM_008020	NP_032046	AAA36563	M75099	86	FK506 binding protein 2	AA684863	3001.8	4062.5	1.4	1.35335
NM_011631	NP_035761	AAK74072	AY040226	90	tumor rejection antigen gp96 (Tra1)	AA685803	6052.4	8526.1	1.4	1.40871
AA799442					Mus musculus 18 days embryo cDNA, RIKEN		1434.7	1983	1.4	1.38217
NM_030986	NP_112248	NP_001616	NM_001625	92	Adenylate kinase 2 (Ak2)	AA799466	707	974.7	1.4	1.37864
X14210	CAA32427	NP_000998	NM_001007	100	ribosomal protein S4.	AA799501	3727.8	5174	1.4	1.38795
AA799525	NP_079634	Q16795	L04490		ESTs, Moderately similar to NUEM_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE 39 KDA SUBUNIT					
AA799550				83	PRECURSOR [H.sapiens]		4954.7	8915.8	1.4	1.79946
AA799551	S06147	O95755	AB023061		Mus musculus RIKEN cDNA 9130413I22 gene		13877.6	19345.2	1.4	1.39399
AA799560				61	ESTs, Weakly similar to S06147 GTP-binding protein rab1B [R.norvegicus]		10159	14085.5	1.4	1.3865
NM_019963	NP_064347	NP_005410	NM_005419		Mus musculus 18 days embryo cDNA, RIKEN		5503.2	9940.1	1.4	1.80624
U52664	AAC05607	AAD01439	AF010472	67	signal transducer and activator of transcription 2 (Stat2)	AA799569	961.8	1312.2	1.4	1.36432
AA799601				88	peptidylglycine alpha-amidating monooxygenase precursor	AA799575	4238.6	8395.2	1.4	1.98065
AA799607					Mus musculus 11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length enriched library, clone:5033430A12		457.9	649.7	1.4	1.41887
AA799645	O08589	O00168	U72245		Mus musculus, clone MGC:12159 IMAGE:3711169		2835.8	3933.1	1.4	1.38695
AA799657				80	FXYD domain-containing ion transport regulator 1		4441.8	8393.1	1.4	1.88957
NM_009087	NP_033113	NP_057056	NM_015972		Mus musculus ERCC2 gene, genomic sequence		1344.2	3109.8	1.4	2.3135
NM_024488	NP_077814	XP_017042	XM_017042	82	RNA polymerase 1-3 (16 kDa subunit) (Rpo1-3),	AA799724	2232.7	3343.8	1.4	1.49765
AA799755	P15087	JC5256	D86479	82	CDK5 activator-binding protein C53 (C53)	AA799745	2635.6	3572.2	1.4	1.35537
AF148216	AAG01898	AAA51851	M14058	84	ESTs, Weakly similar to CARBOXYPEPTIDASE H PRECURSOR [R.norvegicus]		1807.5	1520.3	1.4	0.84111
AA799971				80	serine protease	AA799803	2598	4393.8	1.4	1.69122
					Mus musculus adult male tongue cDNA, RIKEN		3194.3	4507.1	1.4	1.41098

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

AA800036		NP_055390	NM_014575	87n	Schwannomin-interacting protein 1 (SCHIP1)		1811	2957.8	1.4	1.63324
Z83868	CAB06294	NP_061120	NM_018650	87	serine/threonine kinase	AA800063	1391.2	2432.2	1.4	1.74827
X97831	CAA66410	NP_000378	NM_000387	85	carnitine/acylcarnitine carrier protein	AA800120	726	1049.3	1.4	1.44532
AA800168					EST (not recognized)		2126.6	2890.9	1.4	1.3594
AA800176		AAF71034	AF116609	84n	PRO0915	AA800176	1914.8	2761.5	1.4	1.44219
AA800198					Mus musculus adult male tongue cDNA, RIKEN		2992.6	4252.8	1.4	1.42111
NM_013006	NP_037138	NP_008321	NM_008330	86	Lysophospholipase (Lypla1)	AA800220	635.9	891.4	1.4	1.40179
AA800258					Mus musculus adult male tongue cDNA, RIKEN		1315.9	1787.1	1.4	1.35808
AA800318	B26423	ITHUC1	M13203	81	ESTs, Weakly similar to B26423 serine proteinase inhibitor 2.2 - rat [R.norvegicus]		3153.8	4264.9	1.4	1.35231
AA800622					EST (not recognized)		1585.5	2861.4	1.4	1.80473
AA800693					Mus musculus adult male tongue cDNA, RIKEN		448.1	621.8	1.4	1.38764
AA800731					Mus musculus 10 days embryo cDNA, RIKEN		866.2	1234.8	1.4	1.42554
AA800735					Mus musculus, Similar to supervillin, clone IMAGE:3589533		702.7	1017.8	1.4	1.44841
AA800787					Mouse DNA sequence from clone RP23-193O17 on chromosome X		1952.6	2225.2	1.4	1.13961
AA800800					EST (not recognized)		3210.1	4540	1.4	1.41429
NM_019907	NP_063972	NP_054890	NM_014171	99	postsynaptic protein Cript (Cript),	AA818843	4606.3	7545.2	1.4	1.63802
NM_019745	NP_062719	AAH02506	BC002506	96n	programmed cell death 10 (Pdcd10	AA848545	1392.6	2012.6	1.4	1.44521
NM_019745	NP_062719	AAH02506	BC002506	96n	programmed cell death 10 (Pdcd10	AA848546	3523.4	4776.7	1.4	1.35571
AA849648	S26050	JC4916	U43899	96	Ribosomal protein L21		1359.9	2781.2	1.4	2.04515
U50707	AAC52611	NP_003876	NM_003885	89	P35	AA850669	2445.6	3372.2	1.4	1.37888
AA850781	NP_080628	NP_005029	NM_005038	87(mus)	Human peptidylprolyl isomerase D (Rat EST; mouse hypothetical protein)		1572.5	2259.3	1.4	1.43676
AA850940	P50878	P36578	L20868	92	Ribosomal protein L4		8308.7	11979.3	1.4	1.44178
AA859577					Mus musculus, clone IMAGE:3256954		1636.2	2345.8	1.4	1.43369
AA859612					Rattus norvegicus mitochondrial genome	AA859612	5626.4	8004.5	1.4	1.42267
NM_018808	NP_061278	NP_006136	NM_006145	86	DnaJ (Hsp40) homolog, subfamily B, member 1	AA859648	2942.7	3988.4	1.4	1.35467

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

NM_013217	NP_037349	XP_043645	XM_043645	91	afadin (AF-6),	AA859702	1332.1	1931.2	1.4	1.44974
NM_015818	NP_056633	XP_017698	XM_017698	83n	heparan sulfate 6-O-sulfotransferase 1 (Hs6st1)	AA859740	3308	2352.3	1.4	0.71109
AA859760					EST(not recognised)		1397	1938.1	1.4	1.38733
AA859788					Mus musculus adult male brain cDNA, RIKEN		907.7	1248	1.4	1.3749
AA859829					Homo sapiens cDNA FLJ12453 fis, clone NT2RM1000430		2220.7	4847.4	1.4	2.18283
AA859919					Homo sapiens clone 015h12 My015 protein		1403.7	1962.2	1.4	1.39788
AF411216	AAL05859	AAH09758	BC009758	84	vacuole membrane protein 1	AA859954	1547.1	2090	1.4	1.35091
AA860010					Mus musculus, Similar to cholinergic receptor, nicotinic, alpha polypeptide 2 (neuronal), clone MGC:18795 IMAGE:4193582,		1140.8	1580.2	1.4	1.38517
AA860057					Homo sapiens chromosome 5 clone CTC-352M6		723.4	1045.8	1.4	1.44567
AA874889					Homo sapiens mRNA; cDNA DKFZp586D0918 (from clone DKFZp586D0918		1026.9	1418.3	1.4	1.38115
D67015	BAA11034	XP_017163	XM_017163	96	Mouse mRNA for scg	AA874982	1248.6	1719.2	1.4	1.3769
AA875032					EST(not recognised)		470.3	672.4	1.4	1.42973
NM_009838	NP_033968	NP_001753	NM_001762	92	chaperonin subunit 6a (zeta) (Cct6a)	AA875047	2871.3	4115.6	1.4	1.43336
AA875143					Mus musculus adult male tongue cDNA, RIKEN		1216.2	1647.9	1.4	1.35496
AA875171		NP_115909	NM_032520	64	ESTs, Weakly similar to T45062 hypothetical protein c316G12.3 [H.sapiens]		1249.5	1734.2	1.4	1.38792
AA875253					Mus musculus adult male tongue cDNA, RIKEN		3389.3	3690.1	1.4	1.08875
NM_031841	NP_114029	XP_005719	XM_005719	83	stearoyl-CoA desaturase 2	AA875269	29994.5	40736.4	1.4	1.35813
AF140358	AAK98516	NP_004777	NM_004786	97n	thioredoxin-related protein; Trp	AA875390	2862.4	3994.5	1.4	1.39551
NM_019220	NP_062093	NP_001121	NM_001130	80	related to Drosophila groucho gene	AA875427	1054.6	568	1.4	0.53859
AA875506					M.musculus gMCK2alphaC pseudogene		1161.9	1857.9	1.4	1.59902
AA875633					Mus musculus 11 BAC RP23-362J7		29161.2	39715.3	1.4	1.36192
NM_011262	NP_035382	S43202		61	RNA binding motif protein, X chromosome	AA875654	705.9	962.5	1.4	1.36351

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

AA891631					EST (not recognized)		2002	2724.8	1.4	1.36104
AA891677					EST (not recognized)		991.1	1389.2	1.4	1.40167
AA891724		XP_046863	XM_046863	89n	KIAA0699 protein		1061.5	772.7	1.4	0.72793
AA891734					EST(not recognised)		2447.6	4573.6	1.4	1.86861
AF212319	AAG43538	XP_057638	XM_057638	94	NADP+-specific isocitrate dehydrogenase	AA891785	3048.4	4397.2	1.4	1.44246
AF102149					Rattus norvegicus clone ZG52 mRNA sequence.	AA891824	1914.1	2673.3	1.4	1.39664
NM_022948	NP_075237	NP_112233	NM_030971	88	tricarboxylate carrier-like protein (Loc65042),	AA891880	3530.1	4795.4	1.4	1.35843
AA891891		XP_029081	XM_029081	90n	Topoisomerase-related function protein 4-1		777.7	1575.1	1.4	2.02533
AA891902					Mus musculus, clone IMAGE:3585632		1511.3	2052.6	1.4	1.35817
AA891950					Mus musculus adult male stomach cDNA, RIKEN		1141.6	1826.2	1.4	1.59968
AA892154	NP_037292	NP_006445	NM_006454	50	Mad4 homolog (human)		816.6	1105.9	1.4	1.35427
AA892179		XP_040360	XM_040360	89	Similar to chromosome 6 open reading frame 5		1903.1	1518.2	1.4	0.79775
NM_009367	NP_033383			93n	testis expressed gene 261	AA892260	1572.2	2216.4	1.4	1.40974
NM_017470	NP_059498	NP_005731	NM_005740	91n	dynein, axon, light chain 4	AA892303	1478.4	2123.8	1.4	1.43655
AA892378		XP_051242	XM_051242	89n	ESTs, Highly similar to AF151893 1 CGI 135 protein [H.sapiens]		2138	2920.9	1.4	1.36618
AA892414	AAF14345	AAD38322	AF047033	85n	Sodium bicarbonate cotransporter 3 (SLC4A7)		2601	3638.1	1.4	1.39873
AA892417					Mus musculus adult male tongue cDNA, RIKEN		1483.7	1620.7	1.4	1.09234
AB019577	BAA77341	NP_055498	NM_014683	81	UNC-51-like kinase (ULK) 2	AA892500	416	591.6	1.4	1.42212
AA892520					EST(not recognised)		2758.2	3798.6	1.4	1.3772
AA892868					EST(not recognised)		2071.3	3629.3	1.4	1.75218
AA892942					EST (not recognized)		857	1214.2	1.4	1.4168
AA892959					Mus musculus 10 days embryo cDNA, RIKEN		663.5	1491.8	1.4	2.24838
AA892999					EST(not recognised)		1739.2	2435.3	1.4	1.40024
AA893002					EST (not recognized)		3711.8	3440	1.4	0.92677
AA893032					EST (not recognized)		1684.9	2348.2	1.4	1.39367
AA893040					EST (not recognized)		473.3	662.2	1.4	1.39911
AA893043					EST(not recognised)		460.3	627.1	1.4	1.36237
AF133093					Mus musculus X chrom	AA893127	5228.1	7543.5	1.4	1.44288

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

AA893164					Mus musculus, clone IMAGE:3709937		3695	5254.4	1.4	1.42203
AA893183		XP_017866	XM_017866	84n	Homo sapiens hypothetical protein FLJ12529		1043.1	1504.5	1.4	1.44234
AA893217					Human DNA sequence from clone RP11-65K20		5948.9	8398.5	1.4	1.41177
AA893320					EST(not recognised)		1919.6	2702.4	1.4	1.40779
AA893454					EST(not recognised)		1657.3	2363.2	1.4	1.42593
AA893581					Mus musculus RIKEN cDNA 2310004K06		6525.6	9347.2	1.4	1.43239
AA893596	AK016067	AAH03542	BC003542	93(mus)	Mouse RIKEN full-length cDNA		723.4	506.4	1.4	0.70003
AA893659					Homo sapiens cDNA FLJ20789 fis, clone COL01731		1576	2264.6	1.4	1.43693
NM_009183	NP_033209	NP_005659	NM_005668	87n	sialyltransferase 8 (alpha-2, 8-sialytransferase) D (Siat8d)	AA893663	461.4	648.9	1.4	1.40637
AA893664					Homo sapiens BAC clone RP11-334F17		838	1165.9	1.4	1.39129
AA893683					Mus musculus, clone IMAGE:3708747		2571.5	3589.4	1.4	1.39584
NM_019435	NP_062308	NP_061929	NM_019056	79	neuronal protein 15.6 (Np15.6-pending	AA893690	2481.3	3351	1.4	1.3505
NM_007599	NP_031625	NP_001738	NM_001747	89	capping protein (actin filament), gelsolin-like	AA894004	3906.2	5350.2	1.4	1.36967
AA894086					Mus musculus, Similar to CG6769 gene product, clone MGC:6955		679.9	939.9	1.4	1.38241
AA894165					Mus musculus 10 days embryo cDNA, RIKEN		821.2	1183.8	1.4	1.44155
AA894174	AAA41130	P13804	J04058	93	Rat electron transfer flavoprotein (ETF) alpha-subunit DNA, 3' end		2002	2739.3	1.4	1.36828
AA894189					EST (not recognized)		1167.3	1279.5	1.4	1.09612
AA894207		XP_043679	XM_043679	94n	Homo sapiens KIAA1096 protein (KIAA1096), mRNA.		10168.8	14478.1	1.4	1.42378
NM_022542	NP_071987	NP_004031	NM_004040	93n	rhoB gene (Arhb),	AA900505	4065.2	5646.6	1.4	1.38901
AA924809	A41144	JN0503	D11428	86	Peripheral myelin protein		5420.5	7438.8	1.4	1.37235
Y09164	CAA70364	XP_008249	XM_008249	42	sodium channel	AA925248	11864.2	16609.9	1.4	1.4
NM_031621	NP_113809	XP_007014	XM_007014	71	linker of T-cell receptor pathways	AA943555	1924.3	2659.1	1.4	1.38185
NM_022596	NP_072118	XP_005661	XM_005661	60	cis-Golgi matrix protein GM130	AA944423	3370.4	4642.4	1.4	1.3774
X14876	CAA33017	NP_000362	NM_000371	76	transthyretin	AA945169	538.6	745.4	1.4	1.38398
AA955983		NP_002404	NM_002413	81n	microsomal glutathione S-transferase 2 (MGST2),		5263.7	7224.5	1.4	1.37251

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

AA963857	P13265	P51654	U50410	94	Glypican 3		619.2	867.1	1.4	1.40036
NM_017182	NP_058878	NP_004884	NM_004893	89	H2A histone family, member Y (H2afy)	AA965261	211.2	821.3	1.4	3.88873
NM_031731	NP_113919	XP_045058	XM_045058	84	alcohol dehydrogenase family 3, subfamily A2 [	AA996484	1739.6	2403.1	1.4	1.38141
NM_016999	NP_058695	NP_000769	NM_000778	74	Cytochrome P450,	AA997806	2222	3207.4	1.4	1.44347
U25684	AAB37101	NP_068832	NM_021992	60	thymosin beta-like protein	AA997865	557.6	931.6	1.4	1.67073
AB000491	BAA22933	NP_002796	NM_002805	92	proteasome p45/SUG		6617	9023.1	1.4	1.36362
AB000517	BAA22085	XP_003308	XM_003308	86	CDP-diacylglycerol synthase		1827.5	2638.4	1.4	1.44372
AB001347	BAA32473	XP_006487	XM_006487	86	brain beta 3 spectrin		7267.8	10367.5	1.4	1.4265
AB003515	BAA19975	NP_009216	NM_007285	100	GEF-2		10836	16139.9	1.4	1.48947
AB003726	BAA21671	NP_004263	NM_004272	99	Vesl		578.9	991.5	1.4	1.71273
AB003992	BAA20152	NP_003072	NM_003081	100	SNAP-25B		10026.5	16742.5	1.4	1.66982
AB004276	BAA20359	NP_061743	NM_018920	66	protocadherin 4		953.7	1309	1.4	1.37255
AB005549	BAA34216	XP_005858	XM_005858	76	atypical PKC specific binding protein		544.3	750.5	1.4	1.37884
AB006914	BAA22191	NP_004231	NM_004240	78	salt-tolerant protein		1555.4	2446.2	1.4	1.57271
AB009999	BAA28787	XP_003308	XM_003308	88	CDP-diacylglycerol synthase, (18 on d.s.)		3410.4	4106.2	1.4	1.20402
AB010467	BAA28955	AAD01430	AF009670	78	Rattus norvegicus mRNA for multidrug resistance-associated protein (MRP)-like protein-2 (MLP-2), complete cds		484.8	681.2	1.4	1.40512
AB012759	BAA25544	NP_002717	NM_002726	95	prolyl endopeptidase		2221.7	3015.8	1.4	1.35743
AB012933	O88813	JX0202	D10040	62	Acyl-CoA synthetase 5		2468	3484.1	1.4	1.41171
AB013454	R5RT17	R5HU22	X53777	99	ASI mRNA for mammalian equivalent of bacterial large ribosomal subunit protein L22		1063.8	2016.5	1.4	1.89556
AB015191	BAA32440	CAB09722	Z97026	52	Rh blood group protein		649.4	2558.5	1.4	3.93979
AB017655	BAA36838	NP_000730	NM_000739	90	Muscarinic receptor m2		1339.1	1871.8	1.4	1.3978
AB017912	BAA33453	NP_005892	NM_005901	89	Smad2 protein		2240	3049	1.4	1.36116
AF016387	AAD01591	NP_008848	NM_006917	97	retinoid X receptor gamma (RXRgamma)		2638.2	3702.6	1.4	1.40346
AF019974	AAB72089	XP_045588	XM_045588	50	chromogranin B		3649.5	4455	1.4	1.22072
AF022083	AAB82550	AAC78794	AF053356	100	guanine nucleotide binding protein beta 1 subunit		1130.8	1825.9	1.4	1.6147
AF022819	AAD09336	XP_001674	XM_001674	76	Rattus norvegicus putative potassium channel TWIK mRNA		4271.6	4342.1	1.4	1.0165
AF026504	AAB81626	AAC83179	AC004974	81	SPA-1 like protein p1294	AI237576	534.2	770.5	1.4	1.44234

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

AF034582	AAD01990	BAA74928	AB020712	79	Vesicle associated protein (VAP1)		2517.4	3478.9	1.4	1.38194
AF034897	AAC17221	NP_039229	NM_013941	57	olfactory receptor-like protein		506.9	714.7	1.4	1.40994
AF034899	JC5836	Q15062	L35475	44	Olfactory receptor-like protein (SCR D-9)		678.5	689.8	1.4	1.01665
AF036761	AAB88865	AAD29870	AF097514	92	stearoyl-CoA desaturase 2		17628	25494.1	1.4	1.44623
AF044058	AAD13349	AAC36704	AF077953	89	androgen receptor interacting protein; ARIP		1915.1	2614.5	1.4	1.3652
AF053312	P97884	P78556	U77035	61	Small inducible cytokine subfamily A20		465.4	655.9	1.4	1.40933
AF061242	Q9R1B1	Q9Y5J6	AF152355	92	Fracture callus 1		963.4	1349.7	1.4	1.40098
AF074608	AAC33331		no human		MHC class I antigen		6551.3	11434	1.4	1.7453
AF080435	AAC77925	XP_011833	XM_011833	72	phosducin-like protein		1641.3	2974.2	1.4	1.8121
AF091563	AAC64586	AAG45205	AF321237	49	isolate QIL-LD1 olfactory receptor mRNA		1138.1	1568	1.4	1.37773
AF091572	AAC64593	CAA46127	X64994	60	olfactory receptor		1524.5	2081.6	1.4	1.36543
AF091834	AAC61595	NP_006169	NM_006178	100	N-ethylmaleimide sensitive factor NSF		2468.9	3525.3	1.4	1.42788
AF093569	AAD03032	CAB83215	AJ251760	52	XLas protein		1388.7	1944.8	1.4	1.40045
AF095576	AAC64408	BAA22514	AB000520	85n	APS protein		1296.6	1864.4	1.4	1.43791
AF095927	AAC97497	NP_110395	NM_030768	87	Protein phosphatase 2C		2277.7	3138.7	1.4	1.37801
AF096291	1AF3	Q92843	U59747	98	APOPTOSIS REGULATOR BCL-W		1968.2	2694.5	1.4	1.36902
AF104362	AAD04570	NP_005005	NM_005014	75	osteoadherin		917.1	1283.5	1.4	1.39952
M26594	AAA41563	AAB01380	L34035	88	cytosolic malic enzyme	AI008020	2527.9	3554.4	1.4	1.40607
NM_019275	NP_062148	NP_005350	NM_005359	90	MAD homolog 4	AI008639	968.6	1382.1	1.4	1.4269
NM_012839	NP_036971	NP_061820	NM_018947	91	Cytochrome C, expressed in somatic tissues	AI008815	1585.2	2249	1.4	1.41875
NM_022519	NP_071964	NM_000295	NP_000286	66	alpha-1-protease inhibitor	AI010453	1331.3	870.9	1.4	0.65417
NM_031151	NP_112413	NP_005909	NM_005918	89	malate dehydrogenase mitochondrial	AI010480	17460.9	24655.1	1.4	1.41202
NM_031624	NP_113812	NP_001542	NM_001551	77	immunoglobulin (CD79A) binding protein 1	AI011179	1126	1532.1	1.4	1.36066
NM_020075	NP_064460	NP_001960	NM_001969	80	eukaryotic initiation factor 5 (eIF-5)	AI012604	4609.9	6446.5	1.4	1.3984
NM_022713	NP_073204	NP_003232	NM_003241	52	dorsal protein 1	AI013795	533.1	759.9	1.4	1.42544
NM_022585	NP_072107	XP_005226	XM_005226	93	ornithine decarboxylase antizyme inhibitor	AI043631	474.3	914	1.4	1.92705
U89744	AAB49894	XP_003025	XM_003025	50	putative cell surface antigen	AI044259	241.9	4190.2	1.4	17.322
AI044423	P41276	P40616	L28997	98	ADP-ribosylation factor-like 1		4188	3244.2	1.4	0.77464
AF144731	AAD55973	NP_073739	NM_022828	48	putative splicing factor YT521-B	AI044739	638.3	865.7	1.4	1.35626
NM_030990	NP_112252	NP_000524	NM_000533	100	proteolipid protein	AI070277	18303.8	24903.5	1.4	1.36056

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

AI070521	P18395	BAA74908	AB020692	98	Rat unr mRNA for unr protein with unknown function		7164.2	9859.6	1.4	1.37623
M75146		XP_056547	XM_056547	99n	kinesin light chain A	AI073056	33123.6	45656.3	1.4	1.37838
AI073204	P42655	I38947	U20972	98	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activatioprotein, epsilon polypeptide		4345.6	7317.8	1.4	1.68396
Y17323					CDK109	AI102044	27614.4	37985.9	1.4	1.37558
NM_031984	NP_114190	NP_004920	NM_004929	91	cerebellar Ca-binding protein, spot 35 protein; calbindin D28	AI102839	1155.2	1964.9	1.4	1.70092
J01436	AAA99907		no human		cytochrome B gene	AI103396	164178	235960.7	1.4	1.43722
AI103874					Mus musculus 6 days neonate head cDNA, RIKEN		2273	3115.8	1.4	1.37079
AI104389	1TOH	I55282	M20912	88	Tyrosine hydroxylase		1179.9	1701.9	1.4	1.44241
AI104544	R4RT17	R4HU17	M13641	97	Ribosomal protein S17		13022.3	18005.7	1.4	1.38268
NM_022936	NP_075225	XP_005114	XM_005114	71	cytosolic epoxide hydrolase	AI104882	3613	5149.4	1.4	1.42524
AI105463					Mus musculus adult male kidney cDNA, RIKEN		1733.5	2436.5	1.4	1.40554
AI112237					Mus musculus ES cells cDNA, RIKEN		11011.2	14890.2	1.4	1.35228
NM_012637	NP_036769	NP_002818	NM_002827	81	protein-tyrosine phosphatase	AI112391	2560.2	3597.8	1.4	1.40528
NM_017172	NP_058868	NP_004917	NM_004926	78	butyrate response factor 1	AI112516	4385.4	6030.9	1.4	1.37522
M69056	AAA41176	NP_002019	NM_002028	94	farnesyl-protein transferase beta-subunit	AI138396	20	1391.8	1.4	69.59
M36589	AAA41697	XP_002122	XM_002122	86	beta-nerve growth factor	AI137043	884.4	1213.2	1.4	1.37178
AI170379		CAC38839	AJ303079	89n	AKAP-2		1834.2	2546.9	1.4	1.38856
AI171268					Mus musculus adult male kidney cDNA, RIKEN		5236.5	7290.7	1.4	1.39228
AB033713	BAA85626		no human		cytochrome b	AI171355	73530.7	102008.7	1.4	1.38729
NM_017005	NP_058701	XP_050665	XM_050665	90	fumarate hydratase	AI171734	862.1	1168.6	1.4	1.35553
AI175208					Mus musculus 10, 11 days embryo cDNA, RIKEN		1077.1	1486.7	1.4	1.38028
X17215	CAA35084	NP_002219	NM_002228	78	c-jun protein (AA 1-334)	AI175959	2490.2	3506.2	1.4	1.408
NM_009861	NP_033991	NP_001782	NM_001791	100	cell division cycle 42 homolog	AI176308	7113.2	9881.9	1.4	1.38923
AI176422		NP_004444	NM_004453	92	ESTs, Highly similar to 2006241A flavoprotein ubiquinone oxidoreductase [H.sapiens]		1239.1	1789.3	1.4	1.44403
X00722					Rat 32S pre-rRNA 5'-terminal part with 28S rRNA sequence	AI176460	4677.5	7730.4	1.4	1.65268

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

NM_012505	NP_036637	BAA34498	AB018321	99	ATPase, Na+K+ transporting, alpha 2 polypeptide	AI177026	3806.4	5488.9	1.4	1.44202
NM_020075	NP_064460	NP_001960	NM_001969	80	eukaryotic initiation factor 5 (eIF-5)	AI177986	1464.8	1993	1.4	1.3606
AI178204					EST (not recognized)		1091.8	1530.8	1.4	1.40209
NM_031643	NP_113831	NP_002746	NM_002755	90	mitogen activated protein kinase kinase 2	AI178835	980.2	1357.2	1.4	1.38462
AI178921	P35559	P14735	M21188	94	Insulin degrading enzyme		967.3	1627.6	1.4	1.68262
NM_031094	NP_112356	CAA53661	X76061	81	retinoblastoma-like 2 (p130)	AI227715	1690.3	2338.8	1.4	1.38366
AI230294					Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3		870.6	1252.6	1.4	1.43878
NM_010241	NP_034371	NP_071921	NM_022476	96	fused toes	AI230602	4003.1	4976.6	1.4	1.24319
AI232321					Mus musculus 13 days embryo liver cDNA, RIKEN		4300.9	5972.8	1.4	1.38873
X77953	CAA54918	NP_001010	NM_001019	100	ribosomal protein S15a	AI235364	18522.2	28991	1.4	1.5652
U30789					Rattus norvegicus clone N27 mRNA	AI237654	2215.6	3101.5	1.4	1.39985
NM_012598	NP_036730	NP_000228	NM_000237	89	lipoprotein lipase	AI237731	706	957	1.4	1.35552
AI638969					EST(not recognised)		620.2	887.1	1.4	1.43035
AI639032					EST(not recognised)		672.3	955.1	1.4	1.42065
AI639048					Human chromosome 14 DNA sequence BAC C-3028N15 of library CalTech-D		470.5	646.6	1.4	1.37428
AI639058					Mus musculus adult male stomach cDNA, RIKEN		21805.9	30137.6	1.4	1.38208
AI639076					EST (not recognized)		355400.3	507743.3	1.4	1.42865
AI639101					Rattus norvegicus clone RP31-162L19		1130.6	983.8	1.4	0.87016
AI639114					EST(not recognised)		616.4	876.1	1.4	1.42132
AI639120					EST (not recognized)		10972.5	15549.4	1.4	1.41712
NM_007391	NP_031417	XP_006244	XM_006244	71	acrosomal vesicle protein 1 (Acrv1)	AI639153	2092.3	2982	1.4	1.42523
AI639203					EST(not recognised)		1231.8	1963.3	1.4	1.59385
AI639247		AAG49397	AY009106	80	EST, Moderately similar to T17296 hypothetical protein DKFZp434I092.1 [H.sapiens]		2704.5	4663.8	1.4	1.72446
AJ299016	CAC10568	NP_065680	NM_020629	83	receptor tyrosine kinase	AI639318	4404.7	6215.1	1.4	1.41102
AJ131777	CAB66139	NP_006739	NM_006748	79	src-like adaptor protein	AI639338	1153.4	1578.7	1.4	1.36874
AI639343					EST (not recognized)		298	535.9	1.4	1.79832
AF128241	AAD24799	NP_002660	NM_002669	96	pleiotropic regulator 1	AI639353	1944	2726.9	1.4	1.40273
AI639394					EST(not recognised)		444.9	682.2	1.4	1.53338

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

NM_017131	NP_058827	XP_001278	XM_001278	85n	Homo sapiens calsequestrin 1 (fast-twitch, skeletal muscle)	AI639422	3112.3	4343.8	1.4	1.39569
AI639489					Mus musculus 11 days embryo cDNA, RIKEN		986.6	1312.1	1.4	1.35744
AI639516					EST (not recognized)		2708.7	3761.8	1.4	1.38878
AI639524					EST(not recognised)		1058.1	1502.6	1.4	1.42009
AJ005046	CAA06313	NP_003828	NM_003837	95	Rattus norvegicus mRNA for muscle fructose-1,6-bisphosphatase		1520.1	2114.1	1.4	1.39076
AJ006971	CAA07360	NP_001339	NM_001348	72	DAP-like kinase		3269.1	4511	1.4	1.37989
D00729	BAA00629	XP_028848	XM_028848	53	Delta3, delta2-enoyl-CoA isomerase; SEVERAL EXONS; ONLY 1 & 2 LISTED ON THIS SHEET		1053.9	954.6	1.4	0.90578
D10392	1HVV	Q16623	L37792	97	Syntaxin A		2966.7	4227.8	1.4	1.42509
D10655	BAA01504	P10515	Y00978	79	Dihydrolipoamide acetyltransferase		5595.8	7978.2	1.4	1.42575
D10755	BAA01587	XP_046642	XM_046642	100	proteasome subunit R-IOTA		12167.3	16446.5	1.4	1.3517
D10756	BAA01588	XP_042737	XM_042737	98	proteasome subunit R-ZETA		3615.3	5690	1.4	1.57387
D10757	BAA01589	NP_002791	NM_002800	63	proteasome subunit R-RING12		407.6	567.9	1.4	1.39328
D10938	BAA01732	XP_006027	XM_006027	91	brain-derived neurotrophic factor (BDNF)		1155.4	1440.4	1.4	1.24667
D13125	BAA02427	NP_057341	NM_016257	98	neural visinin-like Ca2+-binding protein type 2		1723.9	2495.5	1.4	1.44759
D13556	BAA02754		No Human		T cell receptor eta chain		1163.9	1599.1	1.4	1.37392
D14048	BAA03136	AAH07950	BC007950	91	SP120		2882.7	4087.2	1.4	1.41784
D26439	BAA05455	NP_001757	NM_001766	61	CD1 antigen precursor		929.1	1299.4	1.4	1.39856
D26564	BAA05618	NP_058022	NM_016742	84	Rattus norvegicus mRNA, similar to cdc37		6693.3	9698.9	1.4	1.44905
D30040	BAA06279	XP_015191	XM_015191	98	RAC protein kinase alpha		5684.1	7764.5	1.4	1.366
D30735	BAA06399	CAB87993	AJ238317	85	augmenter of liver regeneration		717.5	1021	1.4	1.423
D30739	BAA06401	NP_003397	NM_003406	99	mitochondrial import stimulation factor (MSF) L subunit		13430.4	18133.8	1.4	1.35021
D42148	BAA07719	NP_000811	NM_000820	79	growth potentiating factor		4732.6	6507.4	1.4	1.37502
D43778	BAA07833	AAA50762	U15592	72	angiotensin II type 2 receptor		808.4	1297.8	1.4	1.60539
D45187	BAA08128	NP_001901	NM_001910	84	cathepsin E precursor		931.9	1318.5	1.4	1.41485
D49955	BAA08710	XP_003594	XM_003594	78	Rat mRNA for bone marrow stromal cell antigen 1 (BST-1)		1845.1	2761.7	1.4	1.49678
D50436	BAA08927	NP_004100	NM_004109	81	adrenodoxin		1347.3	2417.4	1.4	1.79426
D50696	BAA09341	NP_002793	NM_002802	92	proteasomal ATPase (S4)		6848.2	9796.2	1.4	1.43048
D78591	BAA11427	NP_001321	NM_001330	73	cardiotrophin-1		2141.1	2975.4	1.4	1.38966

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

D83948	g1514971	g1469167	D50912	92	S1-1 protein from liver		2535	2471.5	1.4	0.97495
D85189	g2392023	g3158351	AF030555	97	Acyl-CoA synthetase (36 on d.s.)		418.8	708.9	1.4	1.69269
D86557	BAA19880	NP_065172	NM_020439	98	Protein Kinase		1043.1	1488.5	1.4	1.427
D87840	BAA25260	XP_054716	XM_054716	54	Madcam 1		4245.9	5759.6	1.4	1.35651
D88586	P70709	P12724	X15161	55	Rat mRNA for eosinophil cationic protein		5534.2	7523.5	1.4	1.35946
D88672	g2723386	g2781436	AF035483	89	Phospholipase D		739	1056.3	1.4	1.42936
D89514	BAA22837	BAA11559	D82348	91	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase		2210.1	3888.7	1.4	1.75951
D89730	O35568	NP_004096	NM_004105	91	EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (FIBULIN-3) (FIBL-3) (T16 PROTEIN)		2898.6	4009.3	1.4	1.38318
D89983	BAA23594	XP_005226	XM_005226	93	antizyme inhibitor		3259.8	4567.3	1.4	1.4011
D90265	BAA14312	NP_002777	NM_002786	97	proteasome subunit C2		1817.8	3336.1	1.4	1.83524
NM_031154	NP_112416	NP_000839	NM_000848	84	glutathione S-transferase, mu type 3 (Yb3)	E01415	4329.1	5994.2	1.4	1.38463
X13933	CAA32120	AAH08437	BC008437	99	calmodulin (pRCM1).	E02315	70790.7	99823.5	1.4	1.41012
NM_052809	NP_434696	NP_001792	NM_001801	92	cytosolic cysteine dioxygenase 1 (Cdo1),	E03229	1560.7	2161.8	1.4	1.38515
D87671	BAA13432	NP_060918	NM_018448	94	TIP120	E12829	2654.7	3758.5	1.4	1.41579
H31128					EST(not recognised)		2572.1	3648	1.4	1.4183
H31351					EST(not recognised)		1022	1420.7	1.4	1.39012
H31456					EST(not recognised)		3231.1	4533.7	1.4	1.40314
H31535					Mus musculus 10 days embryo cDNA, RIKEN		4411.4	6152.3	1.4	1.39464
H31550					Homo sapiens BAC clone RP11-152F13		4781	6690.1	1.4	1.39931
J00713	AAA40893	AAH05279	BC005279	83	carboxypeptidase a precursor		1887.2	1058.4	1.4	0.56083
J02962	AAA40828	AAA35607	M57710	83	IgE binding protein		6706.6	11005.2	1.4	1.64095
J04629	AAA40782	XP_008232	XM_008232	97	(Na+, K+)-ATPase-beta-2 subunit.		1821.4	2633.6	1.4	1.44592
J05029	AAA40668	NP_001599	NM_001608	87	Acyl Coenzyme A dehydrogenase, long chain		3860.1	6694.2	1.4	1.7342
J05035	AAA42102	NP_001038	NM_001047	63	Steroid 5 alpha-reductase		956.8	1371	1.4	1.4329
J05499	P28492	g4240165	AB020645	76	L-glutamine amidohydrolase		756.7	1375	1.4	1.8171
K02816	AAA41758	NP_006704	NM_006713	66	pR-ET2 encoded oncodevelopmental protein (putative); putative.		9830.9	14225	1.4	1.44697

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

NM_031043	NP_112305	NP_004121	NM_004130	83	glycogenin	L01793	7189.3	8611.9	1.4	1.19788
L02530	AAA41172	NP_001457	NM_001466	94	Drosophila polarity gene (frizzled) homologue		3292	3736.4	1.4	1.13499
L02896	P35053	P35052	X54232	88	Glypican 1		8120.6	11136.1	1.4	1.37134
L07380	NP_036982	XP_030066	XM_030066	79	Growth hormone-releasing factor receptor (16 on d.s.)		3007.6	4107.2	1.4	1.36561
L12382	P16587	P16587	M33384	100	ADP-ribosylation factor 3		2763.6	3824.4	1.4	1.38385
L13202	AAA41319	NP_036315	NM_012183	100	HNF-3/fork-head homolog-2 [Rattus norvegicus] Blink		3557.5	4818.8	1.4	1.35455
L14002					Polymeric immunoglobulin receptor AATTAA-containing 3'UTR mRNA sequence		1206.4	1694.6	1.4	1.40468
L14462	AAC37639	AAC72103	AC005944	80	R-esp1		13161.7	17788.5	1.4	1.35154
L14463	AAC37640	XP_042357	XM_042357	79	transducin		1216.3	1696	1.4	1.39439
L18889	AAA21015	NP_001737	NM_001746	81	calnexin		9848.5	13812.1	1.4	1.40246
L19699	P36860	P11234	M35416	95	Rat GTP-binding protein (ral B) mRNA, complete cds		1676.3	2384.9	1.4	1.42272
L19998	AAA41644	I57945	L19999	74	Minoxidil sulfotransferase		6172.8	8657.8	1.4	1.40257
L21711	AAA65445	XP_039888	XM_039888	70	Galectin-5		634.8	1845	1.4	2.90643
L23148	P41135	JC5396	U57645	90	Inhibitor of DNA binding 1, helix-loop-helix protein (splice variation)		1818.2	2597.6	1.4	1.42867
L24776	OKRTCB	OKHUCB	M34181	91	Tropomyosin non-muscle isoform NM3 (TPM-gamma) mRNA, complete cds		2548.9	3473.6	1.4	1.36278
L26268	AAA85779	NP_001722	NM_001731	99	BTG1; B cell translocation gene		2944.8	4121.7	1.4	1.39965
AF390546	AAK73355	XP_047516	XM_047516	78	gut-enriched kruppel-like factor	L26292	962.2	1393.3	1.4	1.44804
L27124	AAA21818	AAL15441	AY049784	85	NRD convertase		1648.4	2301.4	1.4	1.39614
L27663	A56493	P10586	Y00815	98	POU domain, class 3, transcription factor 2		868.9	779.4	1.4	0.897
L29573	I59558	1707305A	M65105	88	Solute carrier family 6 (neurotransmitter transporter,noradrenalin), member 2		1776.7	2453.1	1.4	1.38071
L33869	AAA40917	NP_000087	NM_000096	82	Ceruloplasmin		1839.2	2507.9	1.4	1.36358
L38483	AAB06509	NP_002217	NM_002226	54	Jagged 1		905	1227	1.4	1.3558
L39018	AAC42059	XP_008249	XM_008249	63	Sodium channel protein 6		1359.2	1932.2	1.4	1.42157
M13979	AAA41248	XP_046330	XM_046330	91	glucose-transporter protein		2408.8	4866	1.4	2.02009
M14656	AAA41762	XP_011125	XM_011125	51	osteopontin		23836	32421.6	1.4	1.36019
M15474	AAA21801	NP_000357	NM_000366	81	Alpha-tropomyosin gene		7266.7	10892.2	1.4	1.49892

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

M17960					insulin-like growth factor II (IGFII)		4025.6	5511.7	1.4	1.36916
M19357	AAA40988	NP_008822	NM_008891	76	Rat gamma-F-crystallin (gamma 4-1) gene, complete cds		1039.3	1503.1	1.4	1.44626
M20721	AAA41950		no human		proline-rich protein		1297.8	1847.7	1.4	1.42372
M22631	AAA88512	NP_000273	NM_000282	89	alpha-propionyl-CoA carboxylase		839.3	1146.1	1.4	1.36554
M22993	AAA79025	NP_002855	NM_002864	60	alpha-1-inhibitor III.		932.6	1325.4	1.4	1.42119
M23264	AAA40759	NP_000035	NM_000044	75	androgen receptor		952.3	1368.3	1.4	1.43684
M23601	AAA41566	NP_000889	NM_000898	83	monoamine oxidase B.		3465.1	4844.6	1.4	1.39811
M23995	AAA40718	P00352	M31994	78	Aldehyde dehydrogenase mRNA, complete cds		4246.9	5755.3	1.4	1.35518
M24104	1SFCA	P19065	AF135372	98	Vesicle-associated membrane protein (synaptobrevin 2)		12034.5	16919.7	1.4	1.40593
M24604					Acc # not recognised		2077.1	2864.2	1.4	1.37894
M24852	AAA41828	AAC00024	U53707	96	neuron-specific protein PEP-19.		13735.2	19867.3	1.4	1.44645
M25350	AAA41846	AAA03589	L20966	96	cAMP phosphodiesterase		546.2	749.4	1.4	1.37202
M25888	AAA41888	NP_000524	NM_000533	100	lipophilin		11803.8	17104.3	1.4	1.44905
M26125	AAA42350	XP_001799	XM_001799	84	epoxide hydrolase		3899.3	5401.4	1.4	1.38522
M26643	AAA41682	XP_008249	XM_008249	83	voltage-sensitive sodium channel alpha subunit.		503.2	681.2	1.4	1.35374
M26686	P22062	P22061	M93008	95	Protein-L-isoaspartate (D-aspartate) O-methyltransferase		4632.1	6554.6	1.4	1.41504
M27293	AAA41384	NP_000866	NM_000875	94	Insulin-like growth factor-I receptor (IGF-I)		2433.3	3484.3	1.4	1.43192
M26837	AAA40641		no human		alpha-2-u globulin	M27434	653.9	919	1.4	1.40541
M27812	AAA42145	XP_013120	XM_013120	64	Synapsin Ia mRNA		3797.2	6451.3	1.4	1.69898
M33025	AAA41810	NP_002815	NM_002824	88	parathymosin		4899.4	6813.4	1.4	1.39066
M33329	AAA42183	AAB23169	S43859	59	hydroxysteroid sulfotransferase a (STa).		652.9	1218.9	1.4	1.8669
M35826	AAA66204		no human		NADH-dehydrogenase (NDI) (att start codon).		97984.1	135553.8	1.4	1.38343
M38135	KHRTH	KHHUH	X16832	82	Cathepsin H		3269.1	4448.2	1.4	1.36068
M55015	AAA41732	XP_048741	XM_048741	73	nucleolin		8965.9	12292.1	1.4	1.37098
M57428	TVRTK6	P23443	M60724	99	S6 kinase		1719.5	2450.6	1.4	1.42518
M58308	AAA63491	NP_002099	NM_002108	92	histidase		948.5	1312.8	1.4	1.38408
M59786	AAA85463	CAA84341	Z34810	85	dihydropryridine-sensitive calcium channel alpha-1 subunit		3584.9	6317.5	1.4	1.76225
M62763	AAA40622	XP_038856	XM_038856	84	60 kDa protein		2476.5	2982.8	1.4	1.20444
M63656	AAA40717	NP_005156	NM_005165	96	aldolase C.		26309.1	36943.5	1.4	1.40421

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

M64301	B40033	Q16659	X80692	97	Mitogen-activated protein kinase 6	2741.4	3119.6	1.4	1.13796
M64376	P23265	g3290001	AC005255	73	Rat olfactory protein	1080.5	1468.2	1.4	1.35882
M65149	AAA40913	NP_005186	NM_005195	81	CELF	1374.7	2363.8	1.4	1.7195
M74223	I56530	g5630085	XM_004826	86	VGF nerve growth factor inducible	3085.9	4335.8	1.4	1.40504
M75153	AAA42012	NP_004654	NM_004663	100	RAB11a, member RAS oncogene family	2318.8	3157.6	1.4	1.36174
M80804	AAA73144	NP_000332	NM_000341	76	Rattus norvegicus unknown mRNA	7923.4	8842.1	1.4	1.11595
M81687	AAA41355	AAA52701	J04621	65	core protein (HSPG)	1069.5	1505.5	1.4	1.40767
M83196	AAB48069	AAD00355	U80458	64	microtubule-associated protein 1A MAP1A	18338.6	24952.7	1.4	1.36067
M83561	AAA02874	AAA95961	U16125	97	Glutamate receptor, ionotropic, kainate 1	1350.2	1833.1	1.4	1.35765
M84210	AAA73182	XP_046406	XM_046406	66	voltage-activating K channel	89.5	2397.1	1.4	26.7832
M86341	Q02589	P54922	L13291	86	ESTs, Highly similar to ADP-RIBOSYLARGININE HYDROLASE [R.norvegicus]	1220	1667.3	1.4	1.36664
M86389	JN0924	HHHU27	L39370	82	Heat shock 27 kDa protein (33 on d.s.)	26712.7	32860.7	1.4	1.23015
M86835	AAA42331	XP_003226	XM_003226	76	Rat vasoactive intestinal polypeptide receptor mRNA	1183.2	1638.1	1.4	1.38447
M88469	AAA41174	BAB18461	AB051390	91	f-spondin	459.6	1025.4	1.4	2.23107
M91599	AAA41157	CAA74200	Y13901	83	fibroblast growth factor receptor subtype 4 (FGFR4)	1116.3	1571.7	1.4	1.40795
M91599	AAA41157	CAA74200	Y13901	83	fibroblast growth factor receptor subtype 4 (FGFR4)	534.4	753.6	1.4	1.41018
M91652	AJRTQ	P15104	Y00387	92	Glutamine synthetase (glutamate-ammonia ligase) (39 on d.s.)	11786.1	16442.8	1.4	1.3951
M92074	AAA42294	NP_000354	NM_000363	75	troponin I.	1779.8	2416.6	1.4	1.35779
M94537	AAA16530	NP_002681	NM_002690	95	Cyclic nucleotide phosphodiesterase (CaM-PDE)	2207.9	3153.1	1.4	1.4281
S46798	AAB23819		no human		ND5	44259.7	60186	1.4	1.35984
S49760	JC6124	Q13574	U51477	92	Diacylglycerol kinase	1076.1	1496.6	1.4	1.39076
S58745	AAB20032	NP_003207	NM_003216	79	Thyrotroph embryonic factor=leucine zipper transcription factor	10480.6	13474.6	1.4	1.28567
S59158	AAB26422	NP_004163	NM_004172	87	glutamate transporter; GluT-1	20	763.4	1.4	38.17
S59525	AAB26420	NP_000397	NM_000406	81	Gonadotropin-releasing hormone receptor	942.5	1282.3	1.4	1.36053
S63519	AAB27415		no human		membrane protein-73; MP-73	2142.5	3074.3	1.4	1.43491
S63521		XP_044201	XM_044201	91n	Glucose-regulated protein GRP78	677.6	971.6	1.4	1.43388

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

S69316									
S75280	AAB33049	XP_038637	XM_038637	92	Rattus sp. 3' UTR.		3580.6	5016.8	1.4	1.40111
S75359	AAB33865	NP_004320	NM_004329	95	pre-mtHSP70		1304.1	1795	1.4	1.37643
S75435	AAB32520	CAA51165	X72500	46	Bone morphogenetic protein type IA receptor		629.8	1147.9	1.4	1.82264
S75997	AAB33384	NP_057637	NM_016553	74	TCR gamma C4L=T-cell receptor gamma chain		6223.5	8452.8	1.4	1.35821
S76466	AAB33045	NP_004293	NM_004302	89	Nucleoporin p62 homolog		2144.7	3017.5	1.4	1.40696
S76779	AAC60703	AAB59397	M10065	73	type I serine-threonine kinase receptor; B1		2332.6	3193.8	1.4	1.3692
S78284	AAC60702	NP_001182	NM_001191	86	apolipoprotein E; ApoE		147033.3	208752	1.4	1.41976
S82649	AAB46783	AAH09924	BC009924	86	apoptosis inducer		2033.6	2921.3	1.4	1.43652
S82911	AAB46839	NP_073207	NM_022716	95	Narp=neuronal activity-regulated pentraxin		2014.5	4482	1.4	2.22487
U05989	AAA16492	AAC24947	U63809	78	rHox= protein		1323.8	2344.2	1.4	1.77081
U07201	P49088	g3341715	AC005326	93	Par-4 induced by effectors of apoptosis		986	1035.7	1.4	1.05041
U08260	I78557	Q14957	L76224	57	Asparagine synthetase		2019.9	2781.5	1.4	1.37705
U09228	AAA21122	AAA60310	M74718	80	Glutamate receptor, ionotropic, N-methyl D-aspartate 2D		1254.9	1711.5	1.4	1.36385
U10995	AAA83437	NP_005645	NM_005654	81	E-box binding factor mRNA		4014.2	4496	1.4	1.12002
U11071					orphan receptor COUP-TFI		605.6	823	1.4	1.35898
U11685	A56043	Q13133	U22662	91	Polyadenylate-binding protein-related protein mRNA, 3' end		318834.4	458301.1	1.4	1.43743
U11760	AAC52154	AAH12195	BC012195	92	Nuclear receptor subfamily 1, group H, member 3		1399.1	1934.2	1.4	1.38246
U14398	:I59355	O00445	X96783	42	transitional endoplasmic reticulum ATPase.		18125.9	24878.7	1.4	1.37255
U14398	:I59355	O00445	X96783	42	Synaptotagmin 4		2308.6	3131.3	1.4	1.35636
U17254	JQ0623	P22736	D49728	91	Synaptotagmin 4		1983.2	2761.2	1.4	1.3923
U17565	AAC18424	NP_005906	NM_005915	91	Immediate early gene transcription factor NGFI-B		3769.3	5176.5	1.4	1.37333
U17901	P54319	g5326866	AF145020	94	Rattus norvegicus intestinal DNA replication protein mRNA, partial cds	AI639082	852.3	720.4	1.4	0.84524
U19485	AAA87903	NP_008875	NM_006944	67	Phospholipase A-2-activating protein (plap)		582.1	832.8	1.4	1.43068
U19614	A56391	CAB43282	AL050126	85	spp-24 precursor		1058.1	1586.4	1.4	1.49929
					Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds		604.2	1532.3	1.4	2.53608

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

U20796	AAA62508	BAA20088	D16815	86	nuclear receptor Rev-ErbA-beta		944.4	1297.8	1.4	1.37421
U26310	AAA67648	NP_072174	NM_022648	97	Tensin (Tns)		5159.6	7447.8	1.4	1.44348
U27201	AAA75002	NP_000353	NM_000362	95	tissue inhibitor of metalloproteinase 3 (TIMP-3		2348.3	4018.8	1.4	1.71137
U27319	AAC52945	NP_000179	NM_000188	100	Hexokinase 1		2906.6	6514.8	1.4	2.24138
U31463	AAA74950	XP_044702	XM_044702	64	nonmuscle myosin heavy chain-A.		2871.9	4026.4	1.4	1.402
U31598	AAA87845	CAA54170	X76775	75	MHC class II-like alpha chain.		3470.1	4784.2	1.4	1.37869
U31668	Q62814	I38878	U15642	95	Transcription factor E2F-5 mRNA, partial cds		310.9	557.7	1.4	1.79382
U32575	AAA85505	AAC09358	AF055006	93	Sec6		1457.9	2017.2	1.4	1.38363
U33553	AAC98537	AAC69612	AF059274	81	Neuroglycan C	E13541	1504.9	2105	1.4	1.39876
U34963	AAA77686	CAA80661	Z23115	88	Programmed cell death repressor BCL-X-Long mRNA		1970.3	2755.9	1.4	1.39872
U36444	AAC52912	NP_006192	NM_006201	92	PCTAIRE-1a protein kinase		2857.6	3991.5	1.4	1.3968
U36895	A57223	AAG10698	AF255342	27	Rattus norvegicus putative pheromone receptor VN3 mRNA, complete cds		705.3	1018.8	1.4	1.44449
U37058	AAA79881	XP_018475	XM_018475	87	neuromedin B receptor		571.2	587.4	1.4	1.02836
U37138	AAC53097	NP_000342	NM_000351	65	Steroid sulfatase (Sts)		1209.9	1668.8	1.4	1.37929
U38801	AAB00389	NP_002681	NM_002690	95	high molecular weight DNA polymerase beta		742.1	1458.7	1.4	1.96564
U39044	AAA89163	AAK37426	AF250307	85	Rattus norvegicus cytoplasmic dynein intermediate chain 2C mRNA, complete cds		1813.8	3370.6	1.4	1.85831
U39549	AAB17890	NP_004702	NM_004711	74	synaptogyrin		2962	2219.2	1.4	0.74922
U49056	AAC52657	XP_046313	XM_046313	50	rA1		1227.3	2670.7	1.4	2.17608
U49062	AAA91470		no human		heat stable antigen CD24		5419	7443.5	1.4	1.37359
U49062	AAA91470		no human		heat stable antigen CD24		2581.6	3518	1.4	1.37336
U50185	AAA92961	XP_028840	XM_028840	37	protein phosphatase 1	AA800549	959.6	1321.3	1.4	1.37693
U50947	AAC52909	NP_003544	NM_003553	55	taste bud receptor protein TB 334.		1275.3	1811	1.4	1.42006
U51583	AAB17130	AAA62155	U19969	75	zinc finger homeodomain enhancer-binding protein-1		793.4	1144	1.4	1.4419
U54632	2016220A	P50550	X96427	99	Ubiquitin conjugating enzyme E2I		1307.2	1876.8	1.4	1.43574
U59241	AAC52855	A42336	M77016	96	E-Tropomodulin		2061.1	2967.9	1.4	1.43996
U60976	AAC98705	NP_005794	NM_005803	81	RAREG-2.1 [		4432.2	6352.3	1.4	1.43322
U61184	AAB03811	NP_001659	NM_001668	81	Aryl hydrocarbon receptor nuclear translocator 1		1251.7	1057.2	1.4	0.84461
U65007	PC4221	TVHUME	M15326	88	Met proto-oncogene		1018.7	1449.5	1.4	1.42289

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

U72620	AAB67042	NP_006709	NM_006718	66	Lot1 (lost on transformation)		1749.1	2498.3	1.4	1.42833
U75210	AAC53160	NP_000229	NM_000238	85	potassium channel protein ERG		3084.2	2712.7	1.4	0.87955
U75405	CAB01633	AAB27856	S64596	84	Collagen alpha1		54964.4	76067.8	1.4	1.38395
U75917	AAB46980	NP_004060	NM_004069	96	clathrin-associated protein 17		7926.3	13762.8	1.4	1.73635
U78102	AAB36783	NP_000390	NM_000399	69	krox20		1716	2342	1.4	1.3648
U79568	AAB50403	XP_008249	XM_008249	63	Voltage-dependent sodium channel PN1 mRNA, partial cds		1216.5	1687.7	1.4	1.38734
U82626	AAB96342	NP_005436	NM_005445	89	Chondroitin sulfate proteoglycan 6		1790	2518.1	1.4	1.40676
U83896	AAB41444	NP_059431	NM_017457	99	yeast sec7B		750.4	1057.3	1.4	1.40898
U88324	P54311	RGHUB1	X04526	100	Guanine nucleotide-binding protein beta		17020.2	23189.1	1.4	1.36245
U90829	AAD09247	NP_003896	NM_003905	96	APP-binding protein 1		1533.4	2216.4	1.4	1.44542
U91561	AAC23707	NP_060599	NM_018129	89	pyridoxine 5'-phosphate oxidase		1052.3	1488.6	1.4	1.41462
X04229	CAA27811	XP_002155	XM_002155	79	glutathione S-transferase (GST) Y(b) subunit		5089.3	6979	1.4	1.37131
X04979	CAA28650	NP_000032	NM_000041	72	Apolipoprotein E		289050	395922.4	1.4	1.36974
X06769	CAA29937	CAA24756	V01512	77	c-fos protein		2221.7	3190.1	1.4	1.43588
X06801	CAA29957	NP_001604	NM_001613	100	vaskular alpha-actin		8166	11572.3	1.4	1.41713
X13016	CAA31438	XP_010594	XM_010594	50	MRC OX-45 surface antigen		2764.2	3880	1.4	1.40366
X13722	CAA32001	AAF24515	AF217403	73	Rat mRNA for LDL-receptor		2079.8	2888.2	1.4	1.38869
X14265	CAA32478	NP_001734	NM_001743	100	calmodulin III		13711.7	19480	1.4	1.42068
X16555	CAA34556	NP_002756	NM_002765	99	ribose-phosphate pyrophosphokinase subunit II		609	833.3	1.4	1.36831
X16933	CAA34808	AAA35781	M94630	81	Rat mRNA for hnRNP C protein, partial		1017.6	1438.1	1.4	1.41323
X53363	CAA37446	NP_004334	NM_004343	85	calreticulin		4606	6412	1.4	1.3921
X54081	CAA38018	NP_001852	NM_001861	79	cytochrome c oxidase subunit IV		25191.1	35621	1.4	1.41403
X54510	P21571	P18859	M37104	76	R.norvegicus mRNA for coupling factor 6 of mitochondrial ATP synthase complex		2848.4	4097.5	1.4	1.43853
X57514	CAA40739	AAD50273	AF165124	71	GABA(A) receptor gamma-1-subunit		1254.4	1716.4	1.4	1.3683
X58865	CAA41674	NP_002618	NM_002627	68	6-phosphofructokinase		2782.4	3855.5	1.4	1.38567
X59864	CAA42524		no human		ASM15 gene		4536.4	6175.6	1.4	1.36134
X60659	CAA43068		no human		potential ligand binding protein		1591.5	2227	1.4	1.39931
X61296	CAA43594		no human		L1 retroposon, ORF2		752.3	810.2	1.4	1.07696
X62841	CAA44645	CAC19684	AL137790	75	voltage-gated potassium channel		20	1786.6	1.4	89.33
D90005					Rat endogenous retroviral sequence, 5' and 3' LTR.	X62951	891	1080	1.4	1.21212

Table 4. Polynucleotide Sequences Which are Upregulated Following Inflammation

X63854	CAA45339	XP_042526	XM_042526	70	mtp2a		1045.7	2694.8	1.4	2.57703
X65454	1908200A	Q92791	U47621	89	SC65 synaptonemal complex protein		1110.2	1025.5	1.4	0.92371
X65948	CAA46766	NP_001505	NM_001514	94	alpha initiation factor		1106.7	1604.4	1.4	1.44972
X66366	CAA47009	XP_012362	XM_012362	96	Gephyrin		1331.2	1865.3	1.4	1.40122
X67250	CAA47672	CAA35769	X51408	97	n-chimaerin		1749.6	4386.6	1.4	2.5072
X68101	CAA48220	XP_048926	XM_048926	87	trg		4248.1	5943.3	1.4	1.39905
X68199	CAA48287	NP_005370	NM_005379	59	myosin I heavy chain		896.5	1232.1	1.4	1.37434
X72757	CAA51286	XP_012265	XM_012265	79	R.norvegicus cox VIa gene (liver)		1050.3	1468.5	1.4	1.39817
X74227	CAA52298	CAB65055	Y18024	68	IP3 3-kinase		1230.5	2109.2	1.4	1.7141
X83579	P51952	P50613	X79193	95	R.norvegicus mRNA for Cdk-activating kinase		494.8	681.8	1.4	1.37793
X95986	g1906814	P16152	J04056	80	Carbonyl reductase		779.8	1070.2	1.4	1.3724
Y00404	CAA68465	NP_000445	NM_000454	83	Copper-zinc-containing superoxide dismutase		25017.8	34713.1	1.4	1.38754
Y12178	CAA72878		No Human		R.norvegicus mRNA for bilitranslocase		528.7	755.8	1.4	1.42954
Y14635	CAA74979	NP_001085	NM_001094	75	proton-gated cation channels modulatory subunit MDEG2		901.2	1235.4	1.4	1.37084
Z11504	CAA77579	NP_000900	NM_000909	86	NPY-1 receptor		1281.9	1843.7	1.4	1.43826
Z36944	S47327	I37242	X77197	98	Putative chloride channel (similar to Mm Clcn4-2)		1371.5	1881.9	1.4	1.37215
NM_020616	NP_065641	NP_065693	NM_020642	70	Mus musculus predicted gene ICRFP703B1614Q5.6	AA799992	1612.2	2301.8	1.4	1.42774
AA893607					Mus musculus, Similar to paxillin, clone IMAGE:3583842		1772.2	2543.7	1.4	1.43533
AI639471					EST (not recognized)		553.2	761.6	1.4	1.37672
D10756	BAA01588	XP_042737	XM_042737	98	proteasome subunit R-ZETA		2092.1	4435	1.4	2.11988
NM_030656	NP_085914	NP_000021	NM_000030	76	Serine-pyruvate aminotransferase	E01050	3276.1	4467.3	1.4	1.3636
J01435					Rattus norvegicus mitochondrial genome		200479.5	289318	1.4	1.44313
NM_031043	NP_112305	NP_004121	NM_004130	83	glycogenin	L01793	4181.2	4557.8	1.4	1.09007

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

Rat Gene Accession. No.	Rat Protein Access. No.	Human Protein Access. No.	Human Gene Access. No.	% homology	Identity	Former Identifier	Naïve Intensity	CFA Intensity	Affymetrix Ratio	Ratio Naïve/CFA
AJ251835					Mus musculus Kcnq1, Ltrpc5, Mash2, Tapa-1, Tssc4 and Tssc6 genes, alternative transcripts	AA799465	1296.5	20	-75.6	64.825
S63521		XP_044201	XM_044201	91n	Glucose-regulated protein GRP78		677.6	20	-24.5	33.88
AF255347	AAK49191	NP_115998	NM_032609	71	Rattus norvegicus cytochrome c oxidase subunit IV isoform 2	H31232	2815.1	20	-22.1	140.755
NM_009394	NP_033420	XP_029894	XM_029894	90n	Mus musculus troponin C, fast skeletal	AI639532	4199.6	20	-20.2	209.98
X00975	CAA25480	AAA91848	M21812	98	MLC2 gene for muscle myosin light chain 2		4708.3	20	-18.9	235.415
NM_011602	NP_035732	AAG39288	AF113217	86n	Mus musculus talin (Tln), mRNA	AA800962	1187.5	20	-18.7	59.375
S69383	AAB30132	NP_001131	NM_001140	70	12-lipoxygenase		4484.6	20	-17.3	224.23
X00975	CAA25480	AAA91848	M21812	98	MLC2 gene for muscle myosin light chain 2		4708.3	20	-18.9	235.415
NM_015818	NP_056633	XP_017698	XM_017698	84(mus)	Mus musculus heparan sulfate 6-O-sulfotransferase 1	AA859740	3308	88.9	-14.1	37.2103487
H33003					EST (not recognized)		3013.4	20	-12.2	150.67
M99223	AAA40991	NP_005164	NM_005173	72	Calcium transporting ATPase mRNA		2466.7	174.2	-11.9	14.1601607
NM_017151	NP_058847	NP_001009	NM_001018	69	Ribosomal protein S15	AA892895	1790.6	20	-11.4	89.53
J04035	Q99372	EAHU	M17282	65	Tropoelastin		4219.6	267.7	-11	15.7624206
X54686	CAA38500	NP_002220	NM_002229	76	R.norvegicus pJunB gene		1795.4	20	-10	89.77
AA875124					EST (not recognized)		2047.8	99.6	-8.9	20.560241
NM_031841	NP_114029	AB032261	BAA93510	92	Stearoyl-CoA desaturase 2	AF036761	6600.8	1035.5	-8.4	6.37450507
L00088	AAA98533	P05976	M20642	85	Rat fast myosin alkali light chains exon 6, common to both MLC1-f and MLC3-f		3003.4	108.2	-8.3	27.7578558
AI230294		XP_004285	XM_004285	90n	Peroxisome proliferative activated receptor, delta [Homo sapiens]		870.6	20	-8.2	43.53
NM_031643	NP_113831	NP_002746	NM_002755	90	Mitogen activated protein kinase kinase 2	AI178835	980.2	20	-8	49.01
S68736	AAB29713	XP_052590	XM_052590	80	Myosin heavy chain mRNA		2188.2	339.3	-6.8	6.44916004
X63143	CAA44848	AAK39969	AF248634	45	neuroglycan		1813.4	20	-6.8	90.67
X16262	CAA34348	NP_002465	NM_002474	88	Myosin heavy chain 21		1045.7	703	-6.7	1.48748222

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

J00692	CAA24534	AAF02694	AF182035	90	Skeletal muscle alpha-actin (original seq withdrawn)		8077	1012.8	-6.6	7.97492101
Z46614	CAA86587	XP_004967	XM_004967	95	Caveolin		1520.1	20	-6.6	76.005
M10140	AAA40935	XP_030967	XM_030967	89	Rat skeletal muscle creatine kinase composite mRNA		11220.6	1503.8	-6.5	7.46149754
S70803	AAB30888			No Human	Clone p10.15 product		3038	468.6	-6.5	6.48314127
AI230260	P13862	P13862	X16312	100	Casein kinase II beta subunit		4209	20	-6.3	210.45
S76489	P52844	P49888	U08098	71	Estrogen sulfotransferase		1933.2	20	-6.2	96.66
U35244	AAC52985	NP_075067	NM_022916	93	vacuolar protein sorting homolog r-vps33a		1057.1	20	-5.9	52.855
BC012962	AAH12962	XP_031260	XM_031260	92n	Mus musculus, Similar to DnaJ (Hsp40) homolog, subfamily B, member 1	AA945704	965.3	20	-5.8	48.265
L35571	A55198	I38522	U07559	72	Insulin related protein 2		852.9	20	-5.5	42.645
X06564	CAA29809	AAB04558	U63041	89	140-kD NCAM polypeptide	AI137246	1012.5	20	-5.5	50.625
AF016047	AAC27973	NP_002564	NM_002573	90	platelet-activating factor acetylhydrolase alpha 1 subunit		4829.2	460.6	-5.3	10.4845853
AI639215					EST (not recognized)		808.7	803.1	-5.3	1.00697298
U52950	AAB17068	NP_005900	NM_005909	89	Microtubule-associated protein 1B mRNA		954.9	20	-5.3	47.745
J04792	AAA66286	NP_002530	NM_002539	91	Ornithine decarboxylase (ODC) gene, complete cds		878.3	20	-5.1	43.915
U19866	AAA68695	NP_056008	NM_015193	92	Growth factor (Arc) mRNA		1072.4	103.2	-4.9	10.3914729
L10362	AAA42189	NP_055663	NM_014848	90	Synaptic vesicle protein 2B (SV2B) mRNA		1122.8	46	-4.8	24.4086957
L21711	AAA65445	XP_039888	XM_039888	70	Galectin-5		634.8	20	-4.8	31.74
NM_008538	NP_032664	XP_039759	XM_039759	84n	Myristoylated alanine rich protein kinase C substrate	AA955167	1089.8	70.1	-4.7	15.5463623
AA859870					EST (not recognized)		1272.1	264.1	-4.6	4.81673608
M91599	AAA41157	NP_002002	NM_002011	83	Rat fibroblast growth factor receptor subtype 4		534.4	54.4	-4.6	9.82352941
D89655	JC5533	A48528	Z22555	78	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1 (scavanger receptor class B type 1)		854.5	20	-4.5	42.725
S80345	AAB35675	NP_000542	NM_000551	87	VHL=von Hippel-Lindau tumor suppressor gene homolog		844.1	20	-4.5	42.205

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

U50353	AAC99551	Human homology too low to include			Defensin 3a (RatNP-3a) gene		3548.3	669.9	-4.5	5.29676071
AA891803	NP_079725	XP_054090	XM_054090	84n	Rat EST; mouse RIKEN protein; human hypothetical protein		1428.1	170.7	-4.3	8.36613943
AA800678					EST(not recognised)		922.7	36.6	-4.2	25.2103825
AI639128		NP_003383	NM_003392	87	Homo sapiens wingless-type MMTV integration site family, member 5A		762.4	20	-4.2	38.12
L24897	AAA72046	XP_052590	XM_052590	86	Rattus norvegicus myosin heavy chain mRNA, 3' end		3814.4	824.4	-4.2	4.62688016
U71293	AAC53018	AAC32258	AF039196	74	Rattus norvegicus hairless protein		1537.2	20	-4.2	76.86
NM_021637	NP_067512	O00506	X99325	92n	Mus musculus serine/threonine kinase 25	AA799791	1541.2	384.6	-4	4.00728029
V01270			M11167	99n	Rattus norvegicus genes for 18S, 5.8S, and 28S ribosomal RNAs	AA859921	15060	6627.3	-4	2.27241863
AI230211	AAA80459	XP_052128	XM_052128	90	Rattus norvegicus voltage-gated K+ channel (Kv43)	AI230211	914.9	396.4	-4	2.3080222
AA859966					Strong homology with 18S rRNA (V01270)		216690.7	55971.4	-3.9	3.87145399
AF002281	AAC16671	XP_003374	XM_003374	88	Alpha-actinin-2 associated LIM protein		620.5	20	-3.9	31.025
S61960	AAB26845	NP_004050	NM_004059	82	Cysteine conjugate beta-lyase		1079.9	268.2	-3.9	4.02647278
AF032120	AAC69268	NP_005707	NM_005716	84	GLUT1 transporter C-terminal binding protein		753.8	73.4	-3.8	10.2697548
J05132	AAA42315	AAG30420	AF297093	78	Rat 3-methylcholanthrene-inducible truncated UDP-glucuronosyltransferase mRNA		778.4	20	-3.8	38.92
NM_012817	NP_036949	NP_000590	NM_000599	96	Insulin-like growth factor-binding protein 5	AI029920	3872.5	1044.3	-3.7	3.70822561
X60469	CAA42999	NP_001155	NM_001164	93	Integrase-like protein, APP interacting protein		1830	488.3	-3.7	3.74769609
AA892645					EST (not recognized)		917.3	255.3	-3.6	3.59302781
AF004811	P31977	A41289	XM_013042	97	Moesin		558.6	41.4	-3.6	13.4927536
NM_022713	NP_073204	XP_044011	XM_044011	52	Rattus norvegicus dorsal protein 1	AI013795	533.1	20	-3.6	26.655
M22400	AAA41735	NP_004475	NM_004484	88	Glypican 3		1290.5	746	-3.6	1.72989276
AA892570					EST (not recognized)		929.8	243.8	-3.5	3.81378179
L19699	AAA42004	AAA60250	M35416	88	Rat GTP-binding protein (ral B)		1936.2	547.8	-3.5	3.53450164
L22557	AAA16633	NP_076951	NM_024046	84	Vesicle-associate calmodulin-binding protein		850.6	168.6	-3.5	5.04507711

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

U16686	AAA91974	Human homology too low to include			Defensin RatNP-1 precursor		1918.2	544	-3.5	3.52610294
X13044	CAA31450	NP_004346	NM_004355	67	MHC-associated invariant chain gamma		6065.3	1467.3	-3.5	4.13364683
X60769	CAA43179	NP_005185	NM_005194	53	Rat sfb mRNA for silencer factor B		587.2	20	-3.5	29.36
M25590	AAA40684		No Human		Androgen-dependent protein precursor	J00791	1305.1	634.3	-3.4	2.05754375
U19614	AAA69914	XP_035429	XM_035429	51	Lamina-associated polypeptide 1C (LAP1C)		2481.3	477	-3.4	5.20188679
U41853	AAB05672	NP_006380	NM_006389	83	150 kDa oxygen regulated protein		868.5	334.2	-3.4	2.59874327
AA892394					EST(not recognised)		1064.2	320.4	-3.3	3.32147316
AI009098		AAH04560	BC004560	92n~	Similar to oxygen regulated protein (150kD)		971	298.7	-3.3	3.25075326
M27726	AAA40815	AAA59597	J03544	92	Phosphorylase (B-GP1)		4948.6	1486.7	-3.3	3.32858008
U17565	AAC18424	NP_005905	NM_005915	91	Intestinal DNA replication protein mRNA, partial cds		852.3	20	-3.3	42.615
U82623	AAB91537	NP_006779	NM_006788	71	cytocentrin		627.3	585.4	-3.3	1.07157499
U91561	AAC23707	NP_060599	NM_018129	89	Pyridoxine 5'-phosphate oxidase		1052.3	323.1	-3.3	3.25688641
X17053	CAA34901	NP_005399	NM_005408	53	Rat immediate-early serum-responsive JE gene		1204.5	741.3	-3.3	1.62484824
M11188			X03205	99	Rat 18S rRNA gene	AA859372	69196	21352.5	-3.2	3.24065098
AA893980					EST(not recognised)		3687.7	4672.8	-3.2	0.78918422
M13508	AAA40748	P06727	X13629	59	Rat apolipoprotein A-IV gene	AA894148	14609.1	4540	-3.2	3.21788344
S83436	AAB50831	AAB50831	S83436	100	Glutahione S-transferase subunit 13	AI105137	1401.1	431.7	-3.2	3.24554088
D87991	BAA13527	NP_005818	NM_005827	84	UDP-galactose transporter related isozyme 1, complete cds		1723.3	815.5	-3.2	2.1131821
AF032667	AAC01579	XP_036173	XM_036173	89	Rexo70		570.9	20	-3.1	28.545
AY028804	AAK83555	XP_050756	XM_050756	84n	Mus musculus golli-interacting protein mRNA	AI229655	1774.8	580.4	-3.1	3.05789111
D13978	BAA03088	AAH08195	BC008195	90	argininosuccinate lyase		587.1	10	-3.1	58.71
NM_019291	NP_062164	NP_000058	NM_000067	80	Carbonic anhydrase II	U60578	1158.1	375.4	-3.1	3.08497603
AA799764					EST(not recognised)		761.4	893.6	-2.9	0.85205909
AB010429	BAA32539	XP_040337	XM_040337	65	Acyl-CoA hydrolase-like protein		1098.6	381.9	-2.9	2.87666929
AF051155	AAD03500	XP_028881	XM_028881	96	G beta-like protein GBL		2859.6	2550	-2.9	1.12141176
H31692				No Human			704.3	402.8	-2.9	1.74851043

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

M61875	AAA53532	XP_030320	XM_030320	69	glycoprotein CD44		1360.1	20	-2.9	68.005
U19614	AAA69914	XP_035429	XM_035429	51	Lamina-associated polypeptide 1C		604.2	897	-2.9	0.6735788
X16481	CAA34501			No Human	Zinc(2+) binding protein		10017.3	6609.9	-2.9	1.51549948
AA892635	TVRTRH	TVHUC4	M31470	99	Ras-like protein		808	283.7	-2.8	2.84807898
AA892801	1606211A	EFHU2	M19997	99	Eukaryotic translation elongation factor 2		15102.3	4362.5	-2.8	3.46184527
AA892916	BAB26060				Rat EST; mouse hypothetical protein from a RIKEN		658.3	171.1	-2.8	3.84745763
NM_012774	NP_036906	NP_004475	NM_004484	88	Glypican 3	AA963857	619.2	111.2	-2.8	5.56834532
U17901	AAA79979	NP_004244	NM_004253	96	Phospholipase A-2-activating protein		582.1	83.3	-2.8	6.9879952
U83896	AAB41444	NP_059431	NM_017457	99	sec7B		750.4	20	-2.8	37.52
NM_030861	NP_110488	NP_002397	NM_002406	84	N-acetylglucosaminyltransferase I	AA957132	627	156.4	-2.7	4.00895141
AF077354	AAC27937	AAA02807	L12723	90	Ischemia responsive 94 kDa protein		685.6	215.4	-2.7	3.18291551
D31873	BAA06672	NP_002305	NM_002314	95	LIMK-1		1533.4	569.4	-2.7	2.69301019
L26525	AAA21089	XP_004559	XM_004559	80	Tyrosine kinase receptor (Ptk-3)		1533.1	566	-2.7	2.70865724
U84030	AAC34734	NP_001939	NM_001948	87	dUTPase		1372.1	516.4	-2.7	2.6570488
AA891802					EST(not recognised)		1163.8	454.7	-2.6	2.55948977
NM_012699	NP_036831	NP_036460	NM_012328	86	Microvascular endothelial differentiation gene 1	AI011998	628.1	114.4	-2.6	5.49038462
U46034	AAC53081	NP_005931	NM_005940	80	Stromelysin 3		750.2	287.8	-2.6	2.6066713
AA799718					Mus musculus ES cells cDNA, RIKEN		1751.2	705	-2.5	2.48397163
NM_009920	NP_034050	NP_005767	NM_005776	59(mus)	Mus musculus comichon (Drosophila) like (Cnil), mRNA	AA866291	836.3	107.2	-2.5	7.80130597
AA866419					EST (not recognized)		590.3	165.6	-2.5	3.56461353
AF257157	AAF72882	NP_036475	NM_012343	88(mus)	Mus musculus nicotinamide nucleotide transhydrogenase	AA891872	635.3	492.2	-2.5	1.29073547
AF020212	AAB71237	NP_036192	NM_012062	72	DLP1 splice variant 2 (DLP1)		519.5	115.3	-2.5	4.50563747
D64045	BAA18932	P27986	M61906	84	Phosphatidylinositol 3-kinase p85 alpha subunit		545.4	135.6	-2.5	4.02212389
X02412	CAA26259	CAA27243	X03541	66	Rat mRNA fragment for striated muscle alpha-tropomyosin		6631.9	2668	-2.5	2.48571984
X53428	CAA37519	NP_002084	NM_002093	95	Glycogen synthase kinase 3 beta		710.1	286.6	-2.5	2.47766923
Y07704	CAA68971	XP_039079	XM_039079	79	Best5 protein		1452.4	589.2	-2.5	2.46503734
AA799726					Mus musculus adult male tongue cDNA, RIKEN		1313.3	550.6	-2.4	2.38521613

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

AA800044					EST(not recognised)		1045.7	239.7	-2.4	4.3625365
AA859942		XP_027016	XM_027016		Homo sapiens N-myristoyltransferase					
				89n	1		2794.1	1206.6	-2.4	2.31568042
AA866231	NP_065813				Rat EST; mouse hypothetical protein from a RIKEN		1429	590.4	-2.4	2.42039295
AA875316					EST(not recognised)		1404.3	446.6	-2.4	3.14442454
AB000928	BAA24486	NP_067009	NM_021186	45	Zona pellucida 1 glycoprotein		3464.8	827.3	-2.4	4.18808171
NM_017187	NP_058883	NP_002120	NM_002129		Rattus norvegicus high mobility group	AI008836				
				91	protein 2		1779.4	726.4	-2.4	2.44961454
AJ010386	CAA09103	XP_043098	XM_043098		ETR-R3b protein, alternatively					
				78	spliced isoform		528.7	136.4	-2.4	3.87609971
AJ012603	CAA10072	NP_003174	NM_003183		TNF-alpha converting enzyme					
				88	(TACE)		1354.8	565.3	-2.4	2.39660357
D14425	BAA03318	NP_000936	NM_000945	100	Calcineurin B		2568	1960.4	-2.4	1.30993875
M36804		XP_006316	XM_006316		Rat follicle stimulating hormone beta-					
				85	subunit mRNA		852.6	362.1	-2.4	2.35459818
M65251	AAA40698	NP_006725	NM_006734		Rat angiotensinogen gene-inducible					
					enhancer-binding protein 1 mRNA, 3'					
				76	end		508	327.1	-2.4	1.55304188
S72407		XP_011387	XM_011387	89	Laminin M subunit		536.6	161.5	-2.4	3.33498452
U09551	AAA53240	XP_027193	XM_027193	89	HMG-box containing protein 1		794.8	333.2	-2.4	2.38535414
X77117					NADH-cytochrome b5 reductase		10338.5	4356.1	-2.4	2.37333854
AA799854					EST (not recognized)		2193.1	20	-2.3	109.655
AA800693					EST (not recognized)		2896.7	1251.7	-2.3	2.31421267
BC004055	AAH04055	XP_011894	XM_011894			AA800735				
				87	Mus musculus, Similar to supervillin		702.7	285.4	-2.3	2.46215837
AA859848	NP_062310				Rat EST; mouse hypothetical protein from a RIKEN		4834.3	2083.8	-2.3	2.31994433
AF057285	AAC97475	XP_034403	XM_034403		Mus musculus intersectin-EH binding	AA893612				
				86n	protein ibp1		5930.5	2617.9	-2.3	2.26536537
U43187	AAB03535	XP_044378	XM_044378		Mus musculus MEK kinase 3, mRNA,	AA925300				
				85n	partial cds		863.5	379.9	-2.3	2.27296657
AF020210	AAB71235	XP_050175	XM_050175		DLP1 splice variant 4 (DLP1) mRNA,					
				83	partial cds		1001.5	428.5	-2.3	2.33722287
AF048828	AAD02476	NP_003365	NM_003374		Rattus norvegicus voltage dependent					
				93	anion channel		1207.1	531.3	-2.3	2.2719744
NM_031020	NP_112282	XP_043351	XM_043351			AI171630				
				94	p38 mitogen activated protein kinase		1355.7	597.6	-2.3	2.2685743
NM_013096	NP_037228			No	Rattus norvegicus Hemoglobin, alpha	AI178971				
				Human	1		5587.8	1966.5	-2.3	2.84149504

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

AI229291			X91648		H.sapiens mRNA for pur alpha					
				92n	extended 3'untranslated region		9346	4130.6	-2.3	2.26262528
AJ224879	CAA12179	CAA29604	X06268							
				93	Collagen alpha 1 type II, partial CDS		3000.1	1303.9	-2.3	2.30086663
L38482	AAA98928	XP_042013	XM_042013	84	Serine protease		6167.4	2703.5	-2.3	2.28126503
M26594	AAA41563	AAB01380	L34035	88	malic enzyme	AI171506	1311.9	572	-2.3	2.29353147
M38566	AAB02287	NP_000775	NM_000784	70	Mitochondrial cytochrome P450		631.7	272	-2.3	2.32242647
S75730	AAB32826	NP_005054	NM_005063		Stearoyl-CoA desaturase 2 SCD2					
				62	homolog		7441.7	2804.6	-2.3	2.65339086
U38253	AAC52788	NP_065098	NM_020365		Initiation factor eIF-2B gamma					
				87	subunit		886.3	290.4	-2.3	3.05199725
U40001	AAC52771	XP_008882	XM_008882		Hormone-sensitive lipase testicular					
				65	isoform		1327.1	20	-2.3	66.355
U95178	AAC33406	XP_003869	XM_003869	80	DOC-2 p59 isoform		793.7	20	-2.3	39.685
X99337	P26453	T17219	T17219							
				95	Stromal cell derived factor receptor 1		816.7	348.2	-2.3	2.3454911
NM_009460	NP_033486	XP_028029	XM_028029			AA686579				
				93n	Mus musculus ubiquitin-like 1 (Ubl1)		914.2	410.7	-2.2	2.22595569
AA799406					EST(not recognised)		10860.4	4394.7	-2.2	2.47124946
AA800808					EST (not recognized)		1355.1	605.5	-2.2	2.23798514
X51974	CAA36236	NP_036254	NM_012122		R.norvegicus mRNA for pI 6.1	AA800851				
				89	esterase		3931.4	1752	-2.2	2.24394977
V01239	CAA24549			No	Rat gene for growth hormone	AA818403				
				Human	(presomatotropin)		617.2	286	-2.2	2.15804196
AA891054					Mouse 4.5S RNA gene		1885	706.8	-2.2	2.66694963
NM_018749	NP_061219	AAH14912	BC014912			AA891553				
					Mus musculus eukaryotic translation					
				92n	initiation factor 3, subunit 7		2460.2	1131	-2.2	2.17524315
AA892801	1606211A	EFHU2	M19997		Eukaryotic translation elongation					
				99	factor 2		12645	5690.2	-2.2	2.22224175
BC012408	AAH12408	NP_001737	NM_001746	87n	Mus musculus, Similar to calnexin	AA893328	822.7	379.9	-2.2	2.16556989
AB008807	BAA34217	NP_004823	NM_004832		glutathione-dependent					
				71	dehydroascorbate reductase		4461.4	20	-2.2	223.07
AF033109	AAC70903	NP_004844	NM_004853	75	syntaxin 8		537.2	245.3	-2.2	2.18997146
AF040750	AAC09272	NP_002073	NM_002082		G protein-coupled receptor kinase 6,					
				88	splice variant C		10142.6	4583.5	-2.2	2.21285044
AI639102					EST(not recognised)		603	277.3	-2.2	2.17454021
U38253	AAC52788	NP_065098	NM_020365		Rattus norvegicus initiation factor eIF-	AI639441				
				87	2B gamma subunit		2794.7	4316.9	-2.2	0.64736586

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

AI639489	AAG45867	XP_035115	XM_035115	85n	Homo sapiens polymerase (DNA directed), delta 3		966.6	440.8	-2.2	2.19283122
D78303	BAA23885	NP_073739	NM_022828	48	YT521 mRNA for RNA splicing-related protein		1112.9	498.3	-2.2	2.23339354
M64300	AAA41124	NP_002736	NM_002745	95	Extracellular signal-related kinase (ERK2)		1610	747.8	-2.2	2.15298208
M75168	AAA41787	NP_004631	NM_004640	98	liver nuclear protein p47		2980.4	1339.7	-2.2	2.22467717
X06701	CAA29887	NP_000509	NM_000518	78	Beta-globin gene	M94919	114847.8	51910.3	-2.2	2.21242798
S83279	AAB49519	NP_000405	NM_000414	83	HSD IV=peroxisome proliferator-inducible gene		3057.3	969.2	-2.2	3.15445728
U54632	AAC98704	NP_003336	NM_003345	100	Rattus norvegicus ubiquitin-conjugating enzyme UbcE2A mRNA		6984.4	2544.8	-2.2	2.73671801
X78848	CAA55405	NP_000838	NM_000847	75	R.norvegicus (Fischer 344) GST Yc1 mRNA		2031.5	1222.7	-2.2	1.66148687
Y07704	CAA68971	XP_039079	XM_039079	79	Best5 protein		1778.5	795.9	-2.2	2.23457721
Z22812	CAA80465	NP_004624	NM_004633	58	Interleukin-1 receptor type 2		1340.8	608.8	-2.2	2.20236531
NM_031648	NP_113836	O00168	U72245	61	Phospholemman chloride channel	AA799645	4441.8	1075.7	-2.1	4.12921818
L47235				No Human	Mus musculus ERCC2 gene	AA799657	1344.2	2096.9	-2.1	0.64104154
AA800024					EST (not recognized)		3834.4	3324.7	-2.1	1.15330707
AA800176		XP_007957	XM_007957	84	Homo sapiens hypothetical protein (LOC57019)		1914.8	916.7	-2.1	2.08879877
AA800671		XP_017730	XM_017730	88	Homo sapiens IQ motif containing GTPase activating protein 2		617.3	219.4	-2.1	2.8135825
AA818726		NP_055152	NM_014337	83n	Homo sapiens peptidylprolyl isomerase (cyclophilin)-like 2		1127.2	537.8	-2.1	2.09594645
L08433				No Human	c-HA-ras proto-oncogene mechanism sequence	AA852046	2473.1	1266.8	-2.1	1.95224187
AA866358					EST (not recognized)		8750.6	4117.1	-2.1	2.12542809
AA866471	AAH08539	BAB14219	AK022744	80(mus)	Unamed protein product		766.5	20	-2.1	38.325
U41803	AAB87720	NP_055689	NM_014874	91	Rattus norvegicus hypertension-related protein	AA874813	6681.8	3189.5	-2.1	2.09493651
AF234783	AAF40439	AAH15221	BC015221	90n	Mus musculus tescalcin mRNA	AA892511	2094.7	1009.2	-2.1	2.07560444
BC009157	AAH09157	XP_009650	XM_009650	91n	N-terminal acetyltransferase complex	AA893199	1268.4	617.1	-2.1	2.05542052
AF026554	O70247	Q9Y289	AF069307	83	Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete cds		1193.5	557.2	-2.1	2.1419598

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

AF031943	AAB87065	NP_001289	NM_001298	90	Rattus norvegicus cyclic nucleotide-gated cation channel (CNG3) mRNA, partial cds		1646.7	791.6	-2.1	2.08021728
AF061945	AAD11811	XP_042803	XM_042803	79	Rattus norvegicus NMDA receptor-like long variant mRNA, partial cds		1031.9	495.8	-2.1	2.08128278
NM_031668	NP_113856	XP_027809	XM_027809	57	MYB binding protein	AI229637	1040.8	493.2	-2.1	2.11030008
NM_012598	NP_036730	NP_000228	NM_000237	89	Lipoprotein lipase	AI237731	706	338.3	-2.1	2.08690511
D10926	BAA01724				Tissue factor pathway inhibitor precursor		879.8	420.2	-2.1	2.09376487
H33459					Mus musculus adult male small intestine cDNA, RIKEN		627.4	305.3	-2.1	2.05502784
M11670	AAA40884	NP_001743	NM_001752	88	Rat liver catalase		1087.6	301.2	-2.1	3.61088977
M31038	AAA41608			No Human	Rat MHC class I non-RT1.A alpha-1-chain		624.9	278.6	-2.1	2.24300072
M77245	B32105	I54360	L13939	96	Adaptor protein complex AP-1, beta 1 subunit		7630.3	3643.9	-2.1	2.0939927
U05013	P23711	I60119	D21243	89	Heme oxygenase-2 non-reducing isoform		1432.7	1961.7	-2.1	0.73033593
U57362	AAB07870	Human homology too low to include			Collagen XII alpha 1 (Col12a1) mRNA, partial cds		1095.2	623.6	-2.1	1.75625401
U76557	AAC53121	XP_047694	XM_047694	88	O-GlcNAc transferase		856.4	288.5	-2.1	2.96845754
X01785	CAA25925	NP_005935	NM_005944	69	Rat thymocyte mRNA for cell surface protein (MRC OX-2)		1240	581.7	-2.1	2.131683
NM_008193	NP_032219	XP_047551	XM_047551	83n	Mus musculus guanylate kinase 1	AA800291	1320.4	672.3	-2	1.98400416
D49708	BAA08556	AAD19278	AF057159	75	RNA binding protein		1249.2	726.4	-2	1.71971366
NM_017248	NP_058944	XP_015755	XM_015755	99	Heterogeneous nuclear ribonucleoprotein A1	AA965147	1234.3	792	-2	1.5584596
AB005540	BAA22332	NP_002586	NM_002595	97	PCTAIRE2		1032.3	523.9	-2	1.9704142
AF004017	AAC40034	AAG47773	AF310248	92	Solute carrier family 4, sodium bicarbonate cotransporter, member 4		2010.8	1029.5	-2	1.95318116
AF044581	AAC18967	XP_039018	XM_039018	87	Syntaxin 13		4772	2446.5	-2	1.95054159
M34464	AAA40683	NP_001625	NM_001634	93	S-adenosylmethionine decarboxylase	AI008131	1410.5	927.9	-2	1.52009915
AI639043					EST (not recognized)		910.4	449.9	-2	2.02356079
AI639159					EST (not recognized)		4794.2	3320.2	-2	1.44394916
J05592	AAA41933	NP_006732	NM_006741	72	Phosphatase inhibitor-1 protein mRNA		1419.1	726.9	-2	1.95226303

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

L18948	AAA18214	NP_002956	NM_002965	64	Intracellular calcium-binding protein (MRP14)		1509.3	631.9	-2	2.38851084
U18314	AAC52209	AAB60330	U09087	79	Rattus norvegicus lamina associated polypeptide 2 (LAP2)		617.6	214.4	-2	2.88059701
U21718		XP_040597	XM_040597	91n	C426 intestinal epithelium proliferating cell-associated mRNA sequence		2819.8	1418.9	-2	1.98731412
U34843	g1236114	g3551742	U27112	93	Rattus norvegicus cell cycle progression related D123 mRNA, complete cds (13 on d.s.)		567.2	256.9	-2	2.20786298
U77931	AAK21974			No Human	rRNA promoter binding protein		13221.3	5476.7	-2	2.41409973
U89743	AAB49893			No Human	Unknown protein mRNA, partial cds		822.4	414.3	-2	1.985035
U95161	AAB54064	AAH02873	BC002873	73	Nuclear protein E3-3 orf2		1195.9	591.2	-2	2.02283491
X06769	CAA29937	CAA24756	V01512	77	c-fos mRNA		2221.7	1111.6	-2	1.99865059
X13044	CAA31450	NP_004346	NM_004355	67	Rat mRNA for MHC-associated invariant chain gamma		5019.5	2489.5	-2	2.01626833
X59864	CAA42524			No Human	Rat ASM15 gene		4536.4	2257.8	-2	2.00921251
X76453	S42794	P53816	X92814	82	Hras-revertant gene 107		2076.4	1023.1	-2	2.02951813
X83537	CAA58521	NP_004986	NM_004995	87	MT-MMP		8321.3	4870.2	-2	1.70861566
AA799497					EST (not recognized)		889.4	461.3	-1.9	1.92802948
X74504	CAA52612			No Human	M.musculus T10 mRNA	AA799663	4649.6	2387.3	-1.9	1.94763959
AA800039	AAH06701	XP_043202	XM_043202	90n	Rat EST; mouse hypothetical protein; Homo sapiens similar to ORF		8833.5	4649.3	-1.9	1.89996344
AA800199	B39066	T34520		73	ESTs, Weakly similar to B39066 proline-rich protein 15 - [R.norvegicus]		3623.5	1871.1	-1.9	1.93656138
AA800673					Mus musculus 10, 11 days embryo cDNA, RIKEN		1412.8	631.2	-1.9	2.2382763
AA859562					EST (not recognized)		1827.2	958.6	-1.9	1.90611308
AA859680					EST (not recognized)		921.7	480.5	-1.9	1.9182102
AA874896					EST (not recognized)		871.7	470.3	-1.9	1.85349777
AA875217					EST (not recognized)		2843.3	1532.6	-1.9	1.85521336
NM_022879	NP_075017	NP_067046	NM_021223	92(mus)	Mus musculus myosin light chain, regulatory A	AA891242	2442.6	1276.4	-1.9	1.91366343
AA892897	1584463	XP_002844	XM_002844	67	Homo sapiens pro[illegible]n-lysine		808.4	423.3	-1.9	1.90975667

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

V01270			M11167	93n	Rattus norvegicus genes for 18S, 5.8S, and 28S ribosomal RNAs	AA893870	52805.4	20689.7	-1.9	2.55225547
AF336828	AAK21297	XP_050453	XM_050453	76	Nucleobindin	AA944007	26790.3	13801.7	-1.9	1.94108697
NM_031603	NP_113791	NP_006752	NM_006761	98	Tyrosine 3-monooxygenase	AA965154	4146.8	2239.9	-1.9	1.85133265
AB000362	BAA19092	NP_001271	NM_001280	98	CIRP (cold-inducible RNA-binding protein)		1364.1	590.2	-1.9	2.31125042
AB013454	BAA34221	NP_003043	NM_003052	69	NaPi-2 beta		1063.8	799.9	-1.9	1.32991624
AF030089	AAD43824		no human		Activity and neurotransmitter-induced early gene protein 4		988.2	508	-1.9	1.94527559
X61043	CAA43378	NP_001393	NM_001402	95	Elongation factor 1 alpha	AI008852	5992.4	3706	-1.9	1.61694549
BC003747	AAH03747	XP_006404	XM_006404	85n	Mus musculus, Similar to troponin T3, skeletal, fast, clone	AI136540	7250.8	4491	-1.9	1.61451792
D38556	BAA07559	NP_000845	NM_000854	78	Rattus norvegicus gene for glutathione S-transferase subunit Yrs	AI138143	2474.3	1336.3	-1.9	1.85160518
BC012522	AAH12522	AAH11890	BC011890	94n	Mouse RIKEN; Homo sapiens, Similar to electron-transferring-flavoprotein dehydrogenase	AI176422	1239.1	381.3	-1.9	3.24967217
AI176589	R5RT27	S43505	L19527	100	Ribosomal protein L27		9047.9	4769.3	-1.9	1.89711278
X52311	CAA36549	XP_032696	XM_032696	92n	Rat unr mRNA for unr protein with unknown function	AI231445	579.2	560.5	-1.9	1.03336307
AI232477	P30670	P30670	AF085709	100	G protein gamma-5 subunit		2587.9	1361.4	-1.9	1.90091083
BC003335	AAH03335	XP_003190	XM_003190	85n	Mus musculus, Similar to replication factor C (activator 1) 4	AI237756	785.3	294.7	-1.9	2.66474381
AI638958					EST (not recognized)		583.2	313.8	-1.9	1.8585086
AI639376		XP_005580	XM_005580	92n	Homo sapiens golgi autoantigen, golgin subfamily a, 1 (GOLGA1), mRNA		762.1	400.6	-1.9	1.90239841
D14014	BAA03115	P24385	X59798	82	Cyclin D1		3068.5	1625.5	-1.9	1.88772685
D49853	LTRT	P41159	U18915	82	Obesity (murine homolog, leptin)		24058.3	14739.3	-1.9	1.63225526
H31982					Rattus norvegicus clone RP31-223K12		1382.3	727.8	-1.9	1.89928552
J02827	AAA40811	NP_000700	NM_000709	86	Branched chain alpha-ketoacid dehydrogenase precursor		580.2	311.5	-1.9	1.86260032
L27128	AAA42110	AAC50804	U34819	97	Rattus norvegicus stress activated protein kinase beta isoform		2279.7	1072.8	-1.9	2.125
M36151	AAA41612	AAA59772	M81141	77	MHC class II A-beta RT1.B-b-beta gene		1111.5	589.1	-1.9	1.88677644
M64986	AAA40729	NP_002119	NM_002128	91	Amphoterin		841.7	20	-1.9	42.085

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

M65149	AAA40913	NP_005186	NM_005195	81	CELF		1374.7	460.1	-1.9	2.98782873
M83681	AAA41998	NP_004274	NM_004283	88	RAB16		532.8	282.4	-1.9	1.88668555
X06701	CAA29887	NP_000509	NM_000518	78	Beta-globin gene	M94918	184613.4	98427.9	-1.9	1.87562063
U11038	AAC52176	NP_002308	NM_002317	72	Lysyl oxidase	S66184	2641.7	1407.1	-1.9	1.87740743
S78215	AAB34333	NP_002699	NM_002708	100	Protein phosphatase 1 alpha		4584.1	2448.1	-1.9	1.87251338
U09793	AAB60458	NP_004976	NM_004985	84	p21		1584.9	837.4	-1.9	1.8926439
U30813					Aspartyl-tRNA synthetase (Psi-DRS1) pseudogene		766.6	218.4	-1.9	3.51007326
U41453	AAD03788	XP_045958	XM_045958	45	PKC binding protein and substrate		4837.4	2499.7	-1.9	1.93519222
U48246	Q62919	Q92832	D83017	92	Protein kinase C-binding protein NELL1		2374	1223	-1.9	1.94112837
U95001	NP_446050	NP_061967	NM_019094	93	Diphosphoinositol polyphosphate phosphohydolase type II (Nudt4)		3927.4	2513.8	-1.9	1.56233591
X07638	A28462	LNHU2A	M11025	67	Asialoglycoprotein receptor 2		525.7	365.2	-1.9	1.43948521
AF019973	AAB72088	CAA31512	X13120	98	Neuron-specific enolase	X07729	9961.6	7507.1	-1.9	1.32695715
X53581					R.norvegicus long interspersed repetitive DNA containing 7 ORF's		8415	4526.6	-1.9	1.85901118
X63375		AAA36352	M25161	87	Beta-1 subunit of Na,K-ATPase		2277.5	1201.2	-1.9	1.89602065
NM_022540	NP_071985	NP_006784	NM_006793	84	Rattus norvegicus peroxiredoxin 3	AA799650	1098.1	611.9	-1.8	1.79457428
AA799732		Q14129	X96484	77	ESTs, Moderately similar to DGCR6 PROTEIN [M.musculus]		2235.3	1217.3	-1.8	1.83627701
AA800290					EST (not recognized)		758.9	250.9	-1.8	3.02471104
AA800772					EST(not recognised)		1076.1	1339.7	-1.8	0.80323953
AB049945	BAB40998	XP_017954	XM_017954	83n	Homo sapiens mitochondrial ribosomal protein S11	AA859788	907.7	516.9	-1.8	1.75604566
AA875500		XP_047123	XM_047123	87n	Homo sapiens KIAA1460 protein		876.4	479.3	-1.8	1.8284999
AA875665	AAH05487	AAH13436	BC013436	88n	Hypothetical protein		4994.7	2129.1	-1.8	2.34592081
AA875665	AAH05487	AAH13436	BC013436	88n	Hypothetical protein		4994.7	2129.1	-1.8	2.34592081
AA891221	NP_080580	XP_051185	XM_051185	96	Hypothetical protein		3754.8	3196.1	-1.8	1.1748068
AA891838	CAB57816	XP_043714	XM_043714	88n	Homo sapiens similar to 60S acidic ribosomal protein PO		3990.9	2228.3	-1.8	1.7910066
AA892250		XP_033978	XM_033978	89n	Homo sapiens lysyl-tRNA synthetase		2016.7	2008.2	-1.8	1.00523378
AF143955	AAD32703	XP_008114	XM_008114	86n	Coronin	AA892506	1705.5	1248.7	-1.8	1.36582045
AA892921		XP_054500	XM_054500	83n	Homo sapiens sorcin (SRI)		2594.7	1431.8	-1.8	1.81219444
AA893032					EST (not recognized)		1684.9	1188.4	-1.8	1.41778862
AA893905		XP_041716	XM_041716	84n	Homo sapiens similar to hypothetical protein FLJ22638		1175.6	453.1	-1.8	2.59457073

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

NM_012963	NP_037095	NP_002119	NM_002128	91	Rattus norvegicus High mobility group 1	AA944177	1746.8	986.9	-1.8	1.76998683
AF014503	AAB94673	NP_036517	NM_012385	63	p8 mRNA		1316.9	738.1	-1.8	1.78417559
AF016252	AAB72005	NP_115984	NM_032595	76	Spinophilin		2717.1	1483.8	-1.8	1.83117671
AF036761	AAB88865	AAD29870	AF097514	92	Stearoyl-CoA desaturase 2		17628	8364.2	-1.8	2.10755362
AF039583	AAC77438	NP_000565	NM_000574	45	Decay-accelarating factor		9201.9	4538.6	-1.8	2.02747543
AI010371					EST (not recognized)		853.9	308.4	-1.8	2.76880674
U05821	AAC52196	NP_001405	NM_001414			AI031019				
				85	Rattus norvegicus translation initiation factor eIF-2B alpha-subunit		1584.2	635.7	-1.8	2.492056
NM_017147	NP_058843	NP_005498	NM_005507	99	Cofilin 1	AI105348	19437.2	10804.6	-1.8	1.79897451
NM_019159	NP_062032	NP_003169	NM_003178	82	Synapsin II	AI145494	828.5	433.4	-1.8	1.91162898
AI170379		CAC38839	AJ303079	89n	Homo sapiens mRNA for AKAP-2 protein		1834.2	1817.4	-1.8	1.00924397
AI175900	P41156	TVHUET	J04101	98	Transcription factor ets-1		1695.4	946.1	-1.8	1.79198816
AI176351	Q64560	P29144	M73047	96	Tripeptidylpeptidase II		932.2	514	-1.8	1.81361868
AI230130	g2648049	AAD40239	AF144748	82	Testicular ecto-ATPase		4006.8	2221.8	-1.8	1.80340265
AI639094					EST (not recognized)		527.4	24.7	-1.8	21.3522267
AF065438	AAC17177	NP_005558	NM_005567	67	Rattus norvegicus mama mRNA	C07012	3452.7	1938.5	-1.8	1.78111942
D10938	BAA01732	XP_006027	XM_006027	91	BDNF		1155.4	854.6	-1.8	1.35197753
H31964					EST (not recognized)		1385.8	783.2	-1.8	1.76940756
J02791	AAA40670	NP_000007	NM_000016							
				86	Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight-chain		1666.5	641.9	-1.8	2.59619878
J05030	AAA40669	NP_000008	NM_000017	86	Rat short chain acyl-coenzyme A dehydrogenase (SCAD)		1620.1	1884.4	-1.8	0.85974315
K02423	AAA98533	XP_030823	XM_030823	85	Rat fast myosin alkali light chain exon 1, specific for MLC1-f		4891.2	2719.6	-1.8	1.79849978
L08491	AAC42030	NP_000798	NM_000807	92	GABA-A receptor alpha-2 subunit		2190.4	1140.6	-1.8	1.92039278
M13100					Long interspersed repetitive DNA sequence LINE3		16447.3	9215.5	-1.8	1.7847431
M61142	g205374	P52888	Z50115	84	Metalloendopeptidase		516.1	282.5	-1.8	1.82690265
M62781	AAA53533	NP_000590	NM_000599	96	Rat insulin-like growth factor binding protein 5		1577.6	2478.6	-1.8	0.63648834
S66618		AAA59575	M14758	85n	Multidrug-resistance transporter P-glycoprotein		1091.5	591.3	-1.8	1.84593269
S74257				No Human	2c9 gene		1324.8	744.6	-1.8	1.77921031

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

U16025	AAA87069	CAA27578	X03945	67	Rattus norvegicus class Ib RT1 mRNA		2461.1	1114.7	-1.8	2.20785862
U17607	AAA91103	BAA12818	D85425	71	Rattus norvegicus CCAAT binding transcription factor CBF subunit C		1031.2	213.6	-1.8	4.82771536
U26356					S100A1 gene		5233.5	1565.9	-1.8	3.34216744
U28975	NP_446270	P48067	S70609	98	Glycine transporter (GLYT-1) gene		969.9	527.6	-1.8	1.83832449
U48596	AAC52596	XP_042066	XM_042066	81	MAP kinase kinase kinase 1 (MEKK1)		864	1624.9	-1.8	0.53172503
U75927		XP_004250	XM_004250	83n	Cytochrome oxidase subunit VIIa mRNA, 3' untranslated region, partial sequence		2880.7	1616.5	-1.8	1.78206001
U90725	AAD09246	A44125	M64098	97	Lipoprotein-binding protein		4473	2457.1	-1.8	1.82043873
X55286	P51639	RDHUE	M11058	92	3-hydroxy-3-methylglutaryl-Coenzyme A reductase		1664.3	710.6	-1.8	2.34210526
X56551	Q02195	P21781	A36301	90	Fibroblast growth factor 7		1720.2	360.7	-1.8	4.76906016
X60351	CAA42910	NP_001876	NM_001885	97	Alpha B-crystallin		19181.4	10581.9	-1.8	1.81266124
X70871	CAA50219	XP_017435	XM_017435	90	Cyclin G		5553.6	3505.4	-1.8	1.58429851
X71466	CAA50583	NP_004521	NM_004530	94	72 KDa type IV collagenase		3721.3	2141.6	-1.8	1.73762607
X97772	CAA66374	XP_010542	XM_010542	92	D-3-phosphoglycerate dehydrogenase		7149.9	4019.7	-1.8	1.77871483
AA799814					EST(not recognised)		915.9	536.9	-1.7	1.70590427
AA799858	P49432	BC000439	AAH00439	83n	Pyruvate dehydrogenase (lipoamide) beta		2371.4	2448.7	-1.7	0.96843223
AA799889	NP_035048	A47328	L04288	56	Natural killer tumor recognition protein (cyclophilin-related)		991.7	582.9	-1.7	1.70132098
NM_011787	NP_035917	AAD56722	AF124145	88n	Mus musculus autocrine motility factor receptor (7TM)	AA800222	3862.6	2247.6	-1.7	1.71854422
NM_017092	NP_058788	AAA19236	U05682	85	Tyro3 (bruton agammaglobulinemia tyrosine kinase)	AA852055	2799.1	1676.6	-1.7	1.66950972
AA874927					EST(not recognised)		8501.1	4861.8	-1.7	1.74854992
AA875198					EST(not recognised)		608.1	105.3	-1.7	5.77492877
AA875620	CAA54424	XP_004187	XM_004187	88	R.norvegicus Hsp70-3 gene (incomplete homology)	AA875620	1187.1	706	-1.7	1.68144476
AA891724		XP_046863	XM_046863	89n	Homo sapiens KIAA0699 protein		1061.5	627.5	-1.7	1.69163347
NM_009671	NP_033801		AK025960	93n	Mus musculus ankyrin repeat hooked to zinc finger motif; Human cDNA	AA891902	519.8	314.4	-1.7	1.65330789
AA892146	AAA40872	XP_003009	XM_003009	76	Carboxypeptidase B gene	AA892146	3186.6	1871.1	-1.7	1.70306237

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

AA892520					EST (not recognized)		2758.2	1653.7	-1.7	1.66789823
AA892548	UBRTA	A23035	X01703	100	Alpha-tubulin		708.2	425.2	-1.7	1.66086548
AA892777	BAB26828	XP_009062	XM_009062							
				84n	Rat EST; mouse hypothetical protein; human hypothetical protein		1501.8	872.6	-1.7	1.72106349
NM_011962	NP_036092	NP_001075	NM_001084	87n	Mus musculus procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	AA892859	1839.5	1069.5	-1.7	1.7199626
NM_011844	NP_035974			No Human	Mus musculus monoglyceride lipase	AA892864	4402.1	2640.6	-1.7	1.66708324
NM_010575	NP_034705	CAA29987	X06831	84n	Mus musculus integrin alpha 2b	AA893733	3197.1	2307.4	-1.7	1.38558551
AA893749					EST (not recognized)		7128.9	4144.2	-1.7	1.72021138
AA893933					EST (not recognized)		2267.9	229.1	-1.7	9.89917067
BC003431	AAH03431	XP_032282	XM_032282	83n	Mus musculus, serine protease inhibitor, Kunitz type 2	AA894130	2625.5	2294.6	-1.7	1.14420814
NM_019147	NP_062020	NP_002217	NM_002226	54	Rattus norvegicus jagged 1 (Jag1)	AA900503	5392.3	3244.4	-1.7	1.66203304
AA925506	I56580	JW0050	AB010414	94	Guanine nucleotide binding protein (G protein), gamma 7 subunit		1285.1	742.1	-1.7	1.73170732
U03490	AAB60489	XP_015728	XM_015728	86n	Phosphocholine cytidylyltransferase	AA925887	813.5	489.1	-1.7	1.66325905
L18891	AAA41637	No human with high enough homology				AA957003				
				95n	Rattus norvegicus intercellular calcium-binding protein (MRP8)		4329.2	2148.1	-1.7	2.01536241
NM_017187	NP_058883	NP_002120	NM_002129	91	Rattus norvegicus high mobility group protein 2	AA996401	2607.1	1143.4	-1.7	2.28012944
S67755	AAB29536	NP_001531	NM_001540	82	Rattus norvegicus heat shock protein 27	AA998683	6673.2	3322.2	-1.7	2.00866895
AB011528	BAA32459	XP_042739	XM_042739	63	MEGF2		1032.6	604.5	-1.7	1.70818859
AB020504	BAA34715			Human too low	PMF31		2277.1	1370.6	-1.7	1.66138917
AF006664	AAB62696	P52952	U34962	87	Rattus norvegicus tinman homolog (rNKx-2.5) mRNA, complete cds		2984.5	4111.5	-1.7	0.72588079
AF034896	AAD01991	NP_039229	NM_013941	57	Olfactory receptor-like protein (SCR D-8)		1871.9	1093.7	-1.7	1.71152987
AF036335	AAD05362	P23246	XM_051944	96	Rattus norvegicus NonO/p54nrb homolog mRNA, partial cds		1916.5	1117	-1.7	1.71575649
AF056324	AAC29479	NP_002958	NM_002967	74	Scaffold attachment factor B		1237.4	741.4	-1.7	1.66900459
AF072411	AAC24876	XP_034144	XM_034144	84	Fatty acid translocase/CD36 mRNA		767.6	456.1	-1.7	1.68286426

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

AF080468	AAC79839	NP_001458	NM_001467		Rattus norvegicus putative glycogen storage disease type 1b protein //					
				93	glucose-6-phosphatase		2489.9	1427.3	-1.7	1.74448259
AF089839	AAC63035	XP_012637	XM_012637		N-ethylmaleimide sensitive factor					
				96	mRNA		608	362.2	-1.7	1.67863059
AF096291	AAC64200	AAB09055	U59747	83	Bcl-w		1968.2	1163.3	-1.7	1.69191094
M27315					Mitochondrial Genome	AI010292	76787.6	40574.5	-1.7	1.89250884
X57228	CAA40505	NP_057535	NM_016451	95	Rat mRNA for beta COP	AI105054	777.1	978.5	-1.7	0.79417476
AI136977	S14538	A46372	M88279		ESTs, Highly similar to P59					
				87	PROTEIN [M.musculus]		5396.1	2497	-1.7	2.16103324
X07268	CAA30252	NP_061821	NM_018948	74	Rat mRNA for gene 33 polypeptide	AI169756	819.3	484.4	-1.7	1.69137077
AI176052	JQ1945	Q9UIJ7	AB021870	89	Adenylate kinase 3		2646.4	1586.3	-1.7	1.66828469
Z78279	CAB01633	AAB27856	S64598	84	Collagen alpha1 type I	AI231472	46998.2	28427.5	-1.7	1.65326532
AF032120	AAC69268	NP_005707	NM_005716		GLUT1 transporter C-terminal binding	AI639271				
				84	protein		9752.8	5787.1	-1.7	1.6852655
AI639347					EST (not recognized)		4824.5	2800.6	-1.7	1.72266657
AJ005984	CAA06798	NP_004427	NM_004436	80	Alpha-endosulfine		2723	1574.9	-1.7	1.72899867
AJ007628	CAA07587	XP_008403	XM_008403	74	ELK channel 1		2936.4	1738.4	-1.7	1.68913944
D00688	BAA00592	NP_000231	NM_000240	82	Monoamine oxidase A		2275.9	1356.1	-1.7	1.67826856
D49395	BAA08388	NP_000860	NM_000869	82	Serotonin 5-HT3 receptor		3331.9	1190.1	-1.7	2.7996807
D85435	BAA36277	AAK97528	AF408198							
				71	Protein kinase C delta-binding protein		2699	1633.9	-1.7	1.65187588
D90211	BAA14236	NP_002285	NM_002294		96 Kd lysosomal membrane					
				58	glycoprotein		4755.6	2842.1	-1.7	1.67326977
L03294	Q06000	LIHUL	M15856	92	Lipoprotein lipase		1752.9	1171.3	-1.7	1.4965423
L13201	AAA74561				HNF-3/forkhead homolog-1		1219	463.1	-1.7	2.63226085
L28801	A56011	I38414	U02619		Rat transcription factor IIIC alpha-					
				77	subunit mRNA, complete cds		10807.1	6497.4	-1.7	1.66329609
L41685	AAB05843	XP_009229	XM_009229		Rattus norvegicus (clone REM3)					
				88	ORF mRNA, partial cds		7107.6	4250.1	-1.7	1.67233712
M13100					Long interspersed repetitive DNA					
					sequence LINE3		3161.2	1881.8	-1.7	1.67988097
M15523	AAA41877	NP_005391	NM_005400		Rat protein kinase C-family related					
				83	mRNA, partial cds, clone RP16		2575.5	1574.4	-1.7	1.63586128
M17412	AAA42232	NP_055182	NM_014367		Growth and transformation-					
				77	dependent protein		3859.4	2279	-1.7	1.69346204
M22670	AAA41592	NP_000005	NM_000014	70	Alpha-2-macroglobulin		1358.9	822.4	-1.7	1.65235895
M36421	AAA41246	CAA41491	X58633	62	Rat glutamate receptor (GluR-D)		1015.2	352.3	-1.7	2.88163497

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

M64797	AAA41163	NP_004558	NM_004567	97	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4		4597.4	871.9	-1.7	5.27285239
M93257				No Human	Cathechol-O-methyltransferase, 3' flank		5819.1	3445.4	-1.7	1.68894758
M96630	AAA42125	XP_043841	XM_043841	100	Homologue to sec61		1861.4	1102.8	-1.7	1.68788538
S58644	AAB26278		No human		Integrin beta 5 subunit		10787.3	6301.6	-1.7	1.71183509
S71570	AAB30870	XP_044348	XM_044348	97	Ca2+/calmodulin-dependent protein kinase II isoform gamma-b		7036.9	4256.5	-1.7	1.65321273
S75280	AAB33049	XP_038637	XM_038637	92	Rattus sp. pre-mtHSP70 mRNA		1304.1	324.4	-1.7	4.02003699
S75359	AAB33865	NP_004320	NM_004329	95	Bone morphogenetic protein type IA receptor		629.8	374.4	-1.7	1.68215812
U02522	AAA82722	NP_004680	NM_004689	89	Mta1 (metastasis associated protein)		687.5	401	-1.7	1.71446384
U14192	AAA62632	NP_003706	NM_003715	83	General vesicular transport factor p115		2293.3	1924.8	-1.7	1.19144846
U24282	AAC52241	P55073	S79854	94	Rattus norvegicus type III iodothyronine deiodinase (dioIII) mRNA		5322.4	4626.5	-1.7	1.15041608
U26397	AAB01069	NP_004018	NM_004027	93	Inositol polyphosphate 4-phosphatase		2449.2	1468.2	-1.7	1.6681651
U52103	AAB03281	XP_011864	XM_011864	92	Rattus norvegicus rCRMP-3 mRNA, partial cds		1908	1124.7	-1.7	1.68645239
U55815	AAC52634	NP_005063	NM_005072	87	Furosemide-sensitive K-Cl cotransporter	U75395	892.1	518.9	-1.7	1.71921372
U72741	P97840	O00182	AB006782	73	Lectin, galactose binding, soluble 9 (Galectin-9)		2183.6	658.2	-1.7	3.31753266
U77583	AAB19228	XP_046995	XM_046995	83	Casein kinase I alpha L		2378.7	1427.8	-1.7	1.66598963
M13101					Rat long interspersed repetitive DNA sequence LINE4		9953.7	5879.4	-1.7	1.69297888
U88036	g2738223	P46721	U21943	72	Brain digoxin carrier protein		2146.5	1291.7	-1.7	1.66176357
U90810	AAB50408	CAA12166	AJ224869	90	CXC chemokine receptor (CXCR4) mRNA		4138.2	2371.2	-1.7	1.74519231
U95052		NP_001409	NM_001418	98	Translation repressor NAT1 mRNA, partial 3'UTR		13013.1	7838.5	-1.7	1.66015181
X05472					Rat 2.4 kb repeat DNA right terminal region		1956.4	1123.6	-1.7	1.74118904
X06554	CAA29797	NP_002352	NM_002361	84	Myelin-associated glycoprotein (S-MAG) C-term		8012.3	3402.4	-1.7	2.35489654

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

X12589	CAA31102	XP_006987	XM_006987	84	Voltage-dependent potassium channel protein		7941.8	4766.4	-1.7	1.6662051
X56325	CAA39764			No Human	2-alpha-1 globin gene		333391.3	175617	-1.7	1.89839993
X77934	CAA54906	NP_001633	NM_001642	79	Amyloid precursor-like protein 2		2482.6	1432.8	-1.7	1.73269123
X95986	CAA65230	NP_001748	NM_001757	83	CBR gene		779.8	446.7	-1.7	1.74569062
Y00350	CAB50784	XP_046565	XM_046565	82	Uroporphyrinogen decarboxylase		2164.7	1246.6	-1.7	1.73648323
Y13413	CAA73837	BAA35188	AB018247	91	Rattus norvegicus mRNA for Fe65L2 protein		1681.7	100.9	-1.7	16.666997
Z78279	CAB01633	AAB27856	S64596	84	Collagen alpha1 type I		28544.1	16544.6	-1.7	1.72528197
AA799473					EST(not recognised)		5190.9	3267.8	-1.6	1.58849991
AA799819					EST (not recognized)		5610.1	4139.6	-1.6	1.35522756
AA800680	BAB28231				EST (mouse hypothetical protein)		4003.9	2518.6	-1.6	1.58973239
AA800684	PT0198	OKHULK	X06369	93	ESTs, Moderately similar to TYROSINE-PROTEIN KINASE LYN [R.norvegicus]		1698.6	1046	-1.6	1.62390057
BC004055	AAH04055	XP_011894	XM_011894	87	Homo sapiens supervillin (SVIL)	AA800735	2777.3	1709.3	-1.6	1.62481718
AA859897		XP_007325	XM_007325	92	Homo sapiens sel-1 (suppressor of lin-12, C.elegans)-like		709.4	449.5	-1.6	1.578198
AA859994			AL110126	92	Human cDNA		709.1	365.9	-1.6	1.93796119
AA875037	S19896	P50453	L40378	76	ESTs, Weakly similar to PLASMINOGEN ACTIVATOR INHIBITOR-2, TYPE A [R.norvegicus]		620.6	2129.6	-1.6	0.29141623
AA875414					EST (not recognized)		1038	663.5	-1.6	1.56443105
NM_031026	NP_112288	NP_006132	NM_006141	90	Rattus norvegicus LIC-2 dynein light intermediate chain 53/55	AA891132	699.5	726.8	-1.6	0.96243808
AA891737					EST (not recognized)		2248.8	1144.2	-1.6	1.96539067
NM_025296	NP_079572	XP_051882	XM_051882	87n	WD40 protein	AA891829	2008.9	1243.5	-1.6	1.61552071
AA892234					EST (not recognized)		22453.4	14227	-1.6	1.5782245
AA892768		XP_034289	XM_034289	91n	Homo sapiens putative breast adenocarcinoma marker (32kD) (BC-2)		2334.3	1417.4	-1.6	1.64688867
AA893443	AAA92787	NP_056461	NM_015646	86	Rap1B		4190.3	2301.9	-1.6	1.82036578
AA893607					EST (not recognized)		1186.3	719.7	-1.6	1.64832569
AA893708					EST (not recognized)		4238.3	2593.7	-1.6	1.63407487
AA893777					EST (not recognized)		1349.7	622.9	-1.6	2.16680045
X00525			M11167	93n	Mouse 28S ribosomal RNA	AA893870	10682.1	6845.4	-1.6	1.56047857

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

AA899106					EST (not recognized)		1167.7	736.8	-1.6	1.58482628
X06801	CAA29957	NP_001604	NM_001613	100	Rat mRNA for vaskular alpha-actin	AA900769	2982.4	2029.7	-1.6	1.46937971
AA944073		Not high enough human homology to include				AA944073				
					R.norvegicus mRNA for ribosomal protein L41		16178.5	9837.8	-1.6	1.64452418
AA946532	P16970	M81182	M81182	95	ATP-binding cassette, sub-family D (ALD), member 3		14485.8	8790.1	-1.6	1.6479676
L14936	AAA41620	NP_109587	NM_030662	86	MAP kinase kinase (MKK2)	AA957896	5233.8	2645.4	-1.6	1.97845316
AA963447		XP_034848	XM_034848	86n	Homo sapiens phosphatase and tensin homolog		1112.7	679.7	-1.6	1.63704576
X65497	CAA46478	XP_037275	XM_037275	87n	R.norvegicus mRNA for poly(ADP-ribose) polymerase	AA964849	2533.7	1573	-1.6	1.6107438
AB016800	BAA34306	XP_006067	XM_006067	82	7-dehydrocholesterol reductase		1953.9	1223.7	-1.6	1.59671488
AF003835	AAC53282	NP_004499	NM_004508	82	Isopentenyl-diphosphate delta isomerase		6614.8	2823.6	-1.6	2.3426831
AF017437	AAB70273	NP_001768	NM_001777	62	Integrin-associated protein		685.6	419.7	-1.6	1.63354777
AF036255	AAC17997	NP_006449	NM_006458	97	RING finger protein		1354	822.5	-1.6	1.64620061
AF048687	AAC24515	XP_008799	XM_008799	91	UDP-Gal:glucosylceramide beta-1,4-galactosyltransferase; beta-1,4-galactosyltransferase		1300.4	798	-1.6	1.62957393
AF055292	AAC12759	XP_043113	XM_043113	90	Signal transducer and activator of transcription 6 (stat6)		2816.8	1425	-1.6	1.97670175
AF062594	AAC67388	NP_004528	NM_004537	57	Nucleosome assembly protein		4689.1	2939.2	-1.6	1.59536609
AF087696	AAC78484	CAB66489	AL136554	97	dlg 2 mRNA, partial cds		1532.5	1101.8	-1.6	1.39090579
AF093268	AAC71032	NP_004263	NM_004272	90	Homer-1c		566.1	360.9	-1.6	1.56857855
AF100421	AAC72405			No Human	LYRIC mRNA		1178.4	716.3	-1.6	1.64512076
BC012408	AAH12408	AAH03552	BC003552	89n	Similar to Calnexin	AI010725	12194.4	7668	-1.6	1.59029734
AF000944	AAB58717	NP_004483	NM_004492	99	TFIIA small subunit mRNA	AI012534	2128.8	1361.1	-1.6	1.56402909
NM_012734	NP_036866	NP_277032	NM_033497	91	Hexokinase 1	AI012593	12557.9	6986.8	-1.6	1.79737505
NM_010887	NP_035017	NP_002486	NM_002495	83	Mus musculus NADH dehydrogenase (ubiquinone) Fe-S	AI013297	4647.1	2279.9	-1.6	2.03629115
AI030175	P27867	Q00798	L29008	82	Sorbitol dehydrogenase		2299.9	1437.5	-1.6	1.59993043
L22079		AAH15065	BC015065	88n	SCAMP 37	AI073164	1209.2	740.6	-1.6	1.63273022
AF117340	AAD25049			No Human	Mus musculus MAP kinase kinase kinase 1	AI102820	1638.9	1040.1	-1.6	1.57571387

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

NM_031099	NP_112361	NP_000960	NM_000969	92	Rattus norvegicus ribosomal protein L5	AI103498	666.8	135.1	-1.6	4.93560326
AI104513	P11240	P20674	M22760	86	Rat CoxVa mRNA for mitochondrial cytochrome c oxidase subunit Va		1318.1	1032.1	-1.6	1.27710493
NM_017172	NP_058868	XP_031094	XM_031094	78	Rattus norvegicus butyrate response factor 1	AI112516	4385.4	2722.3	-1.6	1.61091724
AI137790	Q05310	AAD44484	AF078852	84	R.norvegicus mRNA from Leydig cell hypercalcemic tumour H-500		2039	1294.3	-1.6	1.57536893
M15254	AAA41832	NP_002610	NM_002619	61	Rat platelet factor 4	AI169104	4673.3	2844.1	-1.6	1.64315601
M26594	AAA41563	AAB01380	L34035	88	Rattus norvegicus malic enzyme (MAL) gene	AI171506	989.2	608.7	-1.6	1.62510268
AI177256					EST (not recognized)		3990	2425.8	-1.6	1.6448182
NM_031094	NP_112356	CAA53661	X76061	81	Rattus norvegicus retinoblastoma-like 2 (p130)	AI180396	1841.1	1090.3	-1.6	1.68861781
NM_017212	NP_058908	NP_058518	NM_016834	74	Rattus norvegicus microtubule-associated protein tau	AI227608	21234.3	13506.5	-1.6	1.57215415
NM_019192	NP_062065	CAA77836	Z11793	62	Selenoprotein P, plasma, 1	AI230247	1982.9	1757.9	-1.6	1.12799363
AI639125					EST (not recognized)		1712.7	850.7	-1.6	2.01328318
AI639200					EST(not recognised)		929.5	575	-1.6	1.61652174
AI639225					EST(not recognised)		2045	1293.3	-1.6	1.58122632
AI639294					EST (not recognized)		76817.3	47739.4	-1.6	1.60909647
AI639381			AL138478	88n	EST		1969.1	1238.4	-1.6	1.59003553
AI639391					EST (not recognized)		4424.1	2969.1	-1.6	1.49004749
AI639499					EST (not recognized)		1331	812.2	-1.6	1.63875893
AJ001929	CAA05100	XP_004716	XM_004716	95	CBP-50		8792.9	5442.5	-1.6	1.61559945
D00636	BAA00530	NP_000389	NM_000398	83	NADH-cytochrome b5 reductase		10328.1	5418.7	-1.6	1.90601067
D12519	BAA02089	NP_004594	NM_004603	89	SAP gene for synaptotagmin associated 35kDa		3653.4	2231.7	-1.6	1.63704799
D13376	BAA02643	AAH01116	BC001116	86	Adenylate kinase 1, partial sequence		2260.9	1445.5	-1.6	1.56409547
D14418	BAA21903	AAA35531	M31786	99	A regulatory subunit of protein phosphatase 2A		16995.1	10386.2	-1.6	1.6363155
D16237	BAA03762	NP_068659	NM_021873	74	cdc25B		3662.2	2230	-1.6	1.64224215
D17764	BAA04610	NP_003076	NM_003085	97	Phosphoneuroprotein 14		1850.5	1206	-1.6	1.53441128
D21800	BAA04824	NP_002786	NM_002795	98	Proteasome subunit RC10-II		14259.8	8715.8	-1.6	1.63608619
D28557	BAA05907	AAH09744	BC009744	69	RYB-a		3957.6	2691.1	-1.6	1.47062539
D30804	BAA06463	NP_002783	NM_002792	95	Proteasome subunit RC6-1		6294.1	3910	-1.6	1.60974425

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

D43778	BAA07833	AAA50762	U15592	72	Angiotensin II type 2 receptor	808.4	520.6	-1.6	1.55282367
D45252	BAA08208	NP_002331	NM_002340	82	2,3-oxidosqualene:lanosterol cyclase	4178.7	2021.6	-1.6	2.06702612
D49785	BAA08621	NP_006292	NM_006301	75	Protein kinase (MUK)	2461.6	1834.4	-1.6	1.34191016
D84346	P55161	BAA77295	AB014509	99	NCK-associated protein 1	7268.3	3922.2	-1.6	1.85311815
H33426					EST (not recognized)	1139.7	720.1	-1.6	1.58269885
H33629		XP_016213	XM_018213	91	Homo sapiens hypothetical protein FLJ11046	987.9	845.3	-1.6	1.1686975
J04488	AAA41839	NP_000945	NM_000954	71	Rat prostaglandin D synthetase	25266.2	11750.8	-1.6	2.1501685
L06096	AAA41446	NP_002214	NM_002223	62	Rat inositol trisphosphate receptor subtype 3	6825.7	4345.2	-1.6	1.5708598
L08228	X63255	NP_015566	NM_007327	90	Rattus norvegicus N-methyl-D-aspartate receptor (NMDAR1) gene, exons 1 through 22	3819.7	4713.2	-1.6	0.81042604
L13635	AAA62266	XP_031133	XM_031133	81	Growth response protein (HRS) mRNA	3405.7	2155.5	-1.6	1.58000464
L20869	AAA41809	NP_002571	NM_002580	61	Rat pancreatitis associated protein III	578.7	148.8	-1.6	3.8891129
L22788	AAA57155	NP_001436	NM_001445	78	14 kDa bile acid-binding protein (I-BABP) mRNA	40028.2	24497.1	-1.6	1.63399749
L26267	AAA20684	XP_028204	XM_028204	82	Nuclear factor kappa B p105 subunit	1686.9	20	-1.6	84.345
L31840	AAA74476	NP_065134	NM_020401	88	Nuclear pore complex protein NUP107	2149.9	816.5	-1.6	2.63306797
M17096	AAA42260	No human with high enough homology			Rat transition protein 1 mRNA, complete cds	656.3	843.9	-1.6	0.77769878
M26161	P10499	Q09470	L02750	97	Rattus norvegicus potassium channel protein mRNA, complete cds	2114.5	943.3	-1.6	2.24159864
M57728	AAA41632	XP_054752	XM_054752	83	Rat general mitochondrial matrix processing protease (MPP) mRNA, 3' end	1477.2	917.8	-1.6	1.60950098
M80826	AAA42270	BAA95531	AP001746	68	Intestinal trefoil protein	1524.9	931.7	-1.6	1.63668563
M83107	AAA40762	XP_006432	XM_006432	97	SM22	1082.6	684.7	-1.6	1.58113042
M92340		XP_042068	XM_042068	83n	Rat (clones rLG[08,14,25]) interleukin 6 signal transducer mRNA	1520.1	1104	-1.6	1.37690217

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

M99567	AAK14906	XP_048298	XM_048298	83	Phospholipase C beta-3 mRNA, partial cds		2124.7	1302.4	-1.6	1.63137285
S50879	AAB24586	NP_000656	NM_000665	82	Acetylcholinesterase T subunit		2235.1	1160.1	-1.6	1.92664425
S73007	AAB20688	NP_000336	NM_000345	73	Synuclein SYN1		7893.9	3937.2	-1.6	2.00495276
S75435	AAB32520	AAA61110	M16768	46	TCR gamma C4L=T-cell receptor gamma chain		6223.5	3961.6	-1.6	1.57095618
S78556	AAB34982	XP_038637	XM_038637	93	75 kda glucose regulated protein		6233.1	3884.7	-1.6	1.60452545
S81353	AAB36042	NP_037145	NM_013013	94	Sulfated glycoprotein-1		22254	13827.8	-1.6	1.60936664
U03120	AAA19015	NP_037165	NM_013033	84	Sodium-glucose cotransporter 1		3117.7	1898.3	-1.6	1.64236422
U04738	AAA17519	XP_009594	XM_009594	83	Major hippocampal somatostatin receptor		2598.2	2285.3	-1.6	1.13691857
U11694	AAA91779	AAA60131	J03280	81	Rattus norvegicus WKY and SHRSP phenylethanolamine N-methyltransferase (PNMT) gene	U11275	1631.9	1677.9	-1.6	0.97258478
U11419	AAA50554	NP_000824	NM_000833	52	glutamate receptor		3948.7	1305.9	-1.6	3.02373842
U18314	AAC52209	AAB60330	U09087	79	Lamina associated polypeptide 2 (LAP2)		892.4	559.8	-1.6	1.59414076
U19893	JC7186	XP_029443	XM_029443	98	Alpha actinin 4		3075.7	1931.8	-1.6	1.59214204
J05517	AAA37210	AAH10568	BC010568	87(mus)	Mouse aldolase A gene	U20643	40827	25938.5	-1.6	1.57399233
U30485	AAC52981	NP_001340	NM_001349	94	Aspartyl-tRNA synthetase (DRS1) gene		15613.4	9683.5	-1.6	1.61237156
U36482	AAC15239	NP_006808	NM_006817	91	endoplasmic reticulum protein ERp29 precursor		2757.9	1707.7	-1.6	1.61497921
U44948	AAC52554	NP_001312	NM_001321	88	Rattus norvegicus smooth muscle cell LIM protein		1735.1	1105.1	-1.6	1.57008416
U57042	AAB03110	AAB50235	U90339	90	Adenosine kinase mRNA		3737.3	2403.4	-1.6	1.55500541
U69673	AAC52896	XP_002447	XM_002447	74	Tyrosine phosphatase 20		956.1	1255.1	-1.6	0.76177197
U75393	AAF88164	Homology too low for human			Succinyl-CoA synthetase alpha subunit mRNA nuclear gene encoding mitochondrial protein, partial cds and 3' untranslated sequence		4859.8	2436.8	-1.6	1.99433684
NM_012551	NP_036683	NP_001955	NM_001964	72	Krox-24 mRNA, 3' untranslated region, partial sequence		831.8	514.7	-1.6	1.61608704
U75929				No Human	SPARC mRNA, 3' untranslated region, partial sequence		5380.2	3270.4	-1.6	1.64511986
U75973	AAC53423	XP_027086	XM_027086	86	NAAG-peptidase		1474.2	519.7	-1.6	2.83663652
U88324	AAD00650	NP_002065	NM_002074	95	G protein beta1 subunit (rGb1) mRNA		30804.5	19786.6	-1.6	1.55683644

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

X00722			M11167	96n	Rat 32S pre-rRNA 5'-terminal part with 28S rRNA sequence		5945.5	3762.8	-1.6	1.58007335
X15705	CAA33735	AAD11466	U56725	90	HST protein (AA 1-633)		2521	1549.2	-1.6	1.62729151
X53504	CAA37581	NP_000967	NM_000976	99	Ribosomal protein L12		14415.8	9018.3	-1.6	1.59850526
X53581					R.norvegicus long interspersed repetitive DNA containing 7 ORF's		4575.6	2106.9	-1.6	2.17172149
X57988	CAA41054	NP_000309	NM_000318	88	Peroxisome assembly factor-1	E03344	609.3	378.4	-1.6	1.61020085
X61381	CAA43655	AAH06794	BC006794	65	Interferon induced mRNA		7790.8	4822	-1.6	1.61567814
X62660	CAB46530	NP_000838	NM_000847	56	Glutathione transferase subunit 8		813.8	20	-1.6	40.69
X68199	CAA48287	NP_005370	NM_005379	59	MYR1 mRNA for myosin I heavy chain		896.5	544.2	-1.6	1.64737229
X83399	CAA58316	NP_001959	NM_001968	99	eIF-4E		1391.8	895.9	-1.6	1.5535216
X89383	CAA61563	XP_046267	XM_046267	90	SNF1-related kinase		842.7	534	-1.6	1.57808989
X89963	CAA62002	NP_003239	NM_003248	83	TSP-4 protein		934.6	573.6	-1.6	1.62935844
Y09507	CAA70701	XP_050771	XM_050771	85	Hypoxia-inducible factor 1		862.5	542	-1.6	1.59132841
Z15123		Homology too low for human			S-adenosylmethionine decarboxylase gene, exons 4-8		1969.6	1249	-1.6	1.57694155
Z78279	CAB01633	AAB27856	S64596	84	Collagen alpha1 type I		44177.8	24793.4	-1.6	1.7818371
X14210	CAA32427	NP_000998	NM_001007	100	Rat mRNA for ribosomal protein S4	AA799501	3727.8	2515.8	-1.5	1.48175531
NM_013908	NP_038936			No Human	Mus musculus f-box and WD-40 domain protein 5	AA799654	2914.4	1556.4	-1.5	1.87252634
X87107	CAA60588	AAH04138	BC004138	77	R.norvegicus mRNA for ribosomal protein L6	AA799672	38074.1	26186.7	-1.5	1.453948
NM_009087	NP_033113	XP_040640	XM_040640	92n	Mus musculus RNA polymerase 1-3	AA799724	759.9	502.7	-1.5	1.51163716
AA799773					Mus musculus 18 days embryo cDNA, RIKEN		2027.2	1316.5	-1.5	1.53984049
AF145716	AAF34244	XP_045690	XM_045690	87	Mus musculus SCHIP-1 mRNA	AA800036	1811	1238.8	-1.5	1.46189861
J02650	AAA42071	NP_000972	NM_000981	72	Rattus norvegicus ribosomal protein L19	AA800054	38194.8	25392.2	-1.5	1.5041942
AF364071	AAK50399	NP_055147	NM_014332	81	Rattus norvegicus SMPX protein	AA800221	779.8	535.4	-1.5	1.45648114
AA800535		T47144		29	ESTs, Weakly similar to T47144 hypothetical protein DKFZp761E1347.1 [H.sapiens]		2286.3	936.3	-1.5	2.44184556
AA800686		BAA13198	D86962	88n	Similar to growth factor receptor-binding protein Grb10		1819.2	1111.6	-1.5	1.63655991
NM_012899	NP_037031				Delta - aminolevulinic acid dehydratase (Alad)	AA800745	597.8	409.4	-1.5	1.46018564

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

X14848					Rattus norvegicus mitochondrial genome	AA800849	171420.7	117691.9	-1.5	1.4565208
AA800850		NP_005171	NM_005180	85	murine leukemia viral (bmi-1) oncogene homolog (BMI1),		2173.5	1265.5	-1.5	1.71750296
X14848					Rattus norvegicus mitochondrial genome		2430.2	1635.7	-1.5	1.48572477
NM_008568	NP_032594	XP_036806	XM_036806	87n	Mini chromosome maintenance deficient 7	AA858636	1577.3	1050.9	-1.5	1.50090399
AA859680					EST (not recognized)		4501.6	3092.9	-1.5	1.45546251
AA859757					EST (not recognized)		6171.8	4090.4	-1.5	1.50884999
AA859804		JQ1037	M76477	74	ESTs, Highly similar to SAP3 GANGLIOSIDE GM2 ACTIVATOR PRECURSOR [M.musculus]		1987.3	1354.8	-1.5	1.46685858
AA859909					EST (not recognized)		868.3	579	-1.5	1.49965458
AA859933					EST(not recognised)		897	526.2	-1.5	1.70467503
AA866248					EST (not recognized)		8953.9	4750	-1.5	1.88503158
AA866364					EST (not recognized)		3499	2310.2	-1.5	1.51458748
AA866439					EST (not recognized)		5724.7	3913.1	-1.5	1.46295776
X66209	CAA46960				Rat alpha-2(I) promoter (I)	AA866454	2973.5	2703.2	-1.5	1.0999926
S81497	AAB36043	AAB60328	U08484	72	Lysosomal acid lipase	AA874784	3631.8	923.6	-1.5	3.93222174
D88315	BAA22622	XP_051905	XM_051905	81(mus)	Mouse mRNA for tetracycline transporter-like protein	AA891535	2506.1	1140.3	-1.5	2.19775498
NM_025296	NP_079572	XP_057061	XM_057061	87n	Mus musculus WD40 protein Ciao1	AA891829	2498	1654.9	-1.5	1.50945676
AF219141	AAG37102	XP_030289	XM_030289	88n	Mus musculus nuclear ATP/GTP-binding protein	AA891864	4336.1	2963.9	-1.5	1.46297109
AA891877					Mus musculus 18 days embryo cDNA, RIKEN		1993.6	1314.9	-1.5	1.51616092
AA892325		XP_001428	XM_001428	85n	Homo sapiens choline/ethanolaminephosphotransferase		895.2	826	-1.5	1.08377724
AA892378	NP_079838	XP_051242	XM_051242	89n	Homo sapiens CGI-135 protein (LOC51024); Also listed is Rat EST and mouse hypothetical protein		2138	1469.8	-1.5	1.45461968
AK004841	BAB23608			92n	Mouse RIKEN	AA892789	3489.8	2033.8	-1.5	1.71590127
AA892863					EST (not recognized)		723.7	638.2	-1.5	1.13397054
BC009127	AAH09127			89n	Mouse RIKEN	AA892937	2252.3	1472.5	-1.5	1.52957555
AK013971				84n	Mouse RIKEN	AA893208	2838.5	1885.1	-1.5	1.50575566

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

AA893641	Q9QXQ7	P41221	L20861	98	ESTs, Highly similar to WNT-5A PROTEIN PRECURSOR [R.norvegicus]		2260.5	1490.2	-1.5	1.51691048
X78606	CAA55340	NP_004240	NM_004249	88	R.norvegicus (Sprague Dawley) rab28	AA893673	1145.9	759.8	-1.5	1.50816004
AA894212					EST (not recognized)		2340.4	4322.7	-1.5	0.54142087
NM_017033	NP_058729	XP_046816	XM_046816	94n	Phosphoglucomutase 1	AA894296	4412	3504.9	-1.5	1.2588091
NM_012520	NP_036652	Homology too low for human			Catalase	AA926149	1104.4	749.4	-1.5	1.4737123
AA946439	P02304	P02304	X00038	100	H4 gene for somatic histone H4		2228.9	1100.2	-1.5	2.02590438
AA955477	CAA54183	AAH10407	BC010407	88n	ESTs, Moderately similar to S78100 MAPK-activated protein kinase (EC 2.7.1.-) 2 - mouse (fragment) [M.musculus]		5516.1	1202.6	-1.5	4.58681191
NM_017141	NP_058837	NP_002681	NM_002690	95	Rattus norvegicus DNA polymerase beta	AA957640	5310.6	3601	-1.5	1.47475701
AA958274					EST (not recognized)		616.5	979.2	-1.5	0.62959559
AB000098	BAA24351	XP_009784	XM_009784	54	MIPP65		9399.4	4003.1	-1.5	2.34803028
AB000517	BAA22085	XP_003308	XM_003308	86	CDP-diacylglycerol synthase		1827.5	1186.6	-1.5	1.54011461
AB005143	BAA28832	NP_003346	NM_003355	95	Uncoupling protein 2		5601.8	3628.5	-1.5	1.54383354
AB006607	BAA24366	NP_005189	NM_005198	84	Choline/ethanolamine kinase		2200.9	1738.2	-1.5	1.26619491
AF000423	AAB58344	AAH04291	BC004291	89	Synaptotagmin XI		1752.5	1164.3	-1.5	1.50519626
AF001953	AAB59974	AAG18444	AF300650	99	G protein beta 5 subunit		818.2	541	-1.5	1.51238447
AF003825	AAD09310	AAB61922	U93703	91	GDNF receptor-beta		3274.4	2174.1	-1.5	1.50609448
AF007758	AAC16026	NP_000336	NM_000345	73	Synuclein 1		13291.7	8760.7	-1.5	1.51719611
AF007758	AAC16026	NP_000336	NM_000345	73	Synuclein 1		2902.5	4162.8	-1.5	0.69724705
AF009329	AAB63586	NP_110389	NM_030762	67	Enhancer-of-split and hairy-related protein 1		2198.7	915.5	-1.5	2.40163845
AF020756	AAB94570	AAD42947	AF109387	74	P2X2-3 receptor		7734.2	5329	-1.5	1.45134172
AF044574	AAD02333	NP_065715	NM_020664	83	Putative peroxisomal 2,4-dienoyl-CoA reductase		1056.5	689.3	-1.5	1.53271435
AF047707	AAD02464	NP_003349	NM_003358	95	UDP-glucose:ceramide glycosyltransferase		2400	1554	-1.5	1.54440154
AF061971	AAC16003	NP_005146	NM_005155	87	Palmitoyl-protein thioesterase (PPT-2)		9408.3	6219.9	-1.5	1.51261274
AF076183	AAC31815	XP_006499	XM_006499	90	Cytosolic sorting protein PACS-1a		2152	1397.1	-1.5	1.54033355
AF090867	AAC78657	AAH08281	BC008281	92	Guanosine monophosphate reductase		599.5	411.3	-1.5	1.45757355
AF092450	AAC62110	NP_005447	NM_005456	80	JIP-1 related protein (JIRP)		1684.1	1140.4	-1.5	1.47676254

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

AF096269	AAC79495	XP_045055	XM_045055	77	EH domain binding protein epsin 2		4547.2	2982	-1.5	1.52488263
AF104362	AAD04570	NP_005005	NM_005014	75	Osteoadherin		917.1	594.9	-1.5	1.54160363
NM_012838	NP_036970	NP_000091	NM_000100	78	Rattus norvegicus Cystatin beta	AI008888	10772.9	7249	-1.5	1.48612222
AI071435					Rattus norvegicus Sacm21/RT1-A intergenic region, haplotype RT1n and partial RT1-A gene for MHC Class I antigen	AI071435	1563.9	1036.8	-1.5	1.5083912
AI136891	P17431	Q07352	CAA55670	98	Butyrate response factor 1		6923.2	4917.6	-1.5	1.40784122
NM_012570	NP_036702	NP_005262	NM_005271	92	Glutamate dehydrogenase	AI137421	3123.4	2056.7	-1.5	1.51864638
BC006921	AAH06921	XP_002273	XM_002273	98(mus)	Mus musculus, Inhibitor of DNA binding 2	AI137583	1723.4	967.2	-1.5	1.7818445
Y07744	CAA69024	NP_005467	NM_005476	93	UDP-N-acetyl-D-glucosamine-2-epimerase	AI145931	1847.8	825.9	-1.5	2.23731687
X16956	CAA34830	AAA51811	M17986	72	Rat mRNA for beta-2-microglobulin	AI170268	17154.4	11782.3	-1.5	1.45594663
S75435	AAB32520	AAA61110	M16768	46	TCR gamma C4L=T-cell receptor gamma chain	AI176307	4663.5	3204.3	-1.5	1.45538807
AF369384	AAK53428	NP_002749	NM_002758	97	Mitogen-activated protein kinase kinase 6	AI176689	2941.3	1998.4	-1.5	1.47182746
AF237622	AAF73953	XP_040744	XM_040744	93n	Mus musculus acetyltransferase Tubedown-1	AI177404	1344.7	895.7	-1.5	1.50128391
Y16641	CAA76339	Homology too low for human			Rattus norvegicus mRNA for hnRNP protein	AI177683	2127.2	1432.6	-1.5	1.48485272
NM_020075	NP_064460	NP_001960	NM_001969	80	Rattus norvegicus eukaryotic initiation factor 5	AI177986	1464.8	996.7	-1.5	1.46964984
X16417	CAA34439	NP_000509	NM_000518	81	Rat mRNA for beta-globin	AI179576	211405.1	145499.8	-1.5	1.45295801
AI179916		XP_018277	XM_018277	94n	Homo sapiens similar to PNAS-106		2293.5	1534.1	-1.5	1.49501336
NM_020079	NP_064484	CAA38264	X54393	28	Rattus norvegicus Prolactin-like protein C	AI180410	1106.4	713.6	-1.5	1.55044843
U07683	AAA50212	AAC50565	U30930	93	Rattus norvegicus UDP-galactose:ceramide galactosyltransferase	AI228110	10596.6	7218.4	-1.5	1.46799845
BC004827	AAH04827	Homology too low for human			Similar to phosphoserine aminotransfe	AI230228	2597.1	1409.9	-1.5	1.84204554
AK004782	BAB23560				Mouse RIKEN	AI232691	.1067	701.5	-1.5	1.52102637
BC002124		XP_056180	XM_056180	96n	Mus musculus, Similar to RNA binding motif protein 9	AI638955	3114.8	2114.9	-1.5	1.47278831
AI639112					EST(not recognised)		994.5	658.3	-1.5	1.5107094
NM_007704	NP_031730	BAB19683	AB044807	77(mus)	Mus musculus channel-interacting PDZ domain protein	AI639123	1479.3	996.6	-1.5	1.48434678

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

U13371					Mouse Clone	AI639149	1166.3	768.4	-1.5	1.51782926
NM_019953	NP_064337	NP_055070	NM_014255	88n	Mus musculus transmembrane protein 4	AI639208	1855.3	1208.7	-1.5	1.53495491
NM_028785	NP_083061				Mouse RIKEN	AI639255	4324.4	2815	-1.5	1.53619893
AI639372		XP_053842	XM_053842	89n	Homo sapiens KIAA0854 protein		3386.3	1385.6	-1.5	2.44392321
AI639387					EST(not recognised)		1045.9	715.9	-1.5	1.46095823
BC002306	AAH02306	AAH00739	BC000739	88n	Mus musculus, Similar to CG11246 gene product	AI639518	5007.1	3439.3	-1.5	1.45584857
AJ000347	CAA04022	NP_006076	NM_006085	91	Rattus norvegicus mRNA for 3'(2'),5'-bisphosphate nucleotidase		3080.5	2085.7	-1.5	1.47696217
AJ007291	CAA07434	XP_042309	XM_042309	91	CAP1 gene		15227	10082	-1.5	1.51031541
AJ007632	CAA07591	XP_008403	XM_008403	61	ELK channel 3		1821.8	1246.4	-1.5	1.48164855
D10699	BAA01541	XP_051781	XM_051781	95	Ubiquitin carboxyl-terminal hydrolase		74133	50093.7	-1.5	1.47988669
D10729	BAA01572	XP_016879	XM_016879	93	Proteasome subunit RC1		1799.1	1165.1	-1.5	1.5441593
D12498	BAA02059	XP_016079	XM_016079	91	FGF receptor-1		4477.1	3083.6	-1.5	1.45190686
D12769	BAA02236	NP_001197	NM_001206	91	BTE binding protein		1318.4	2120.6	-1.5	0.62171084
D12769	BAA02236	NP_001197	NM_001206	91	BTE binding protein		951.1	972	-1.5	0.97849794
D17521	BAA04471	NP_001820	NM_001829	90	Protein kinase C-regulated chloride channel		5493.9	3580.2	-1.5	1.53452321
D21869	BAA21013	AAH07798	BC007798	96	PKF-M (phosphofructokinase-M)		4316.8	2941.4	-1.5	1.46760046
D38560	BAA18911	XP_003450	XM_003450	85	CyclinG-associated kinase		1064.2	704.1	-1.5	1.51143304
D44495	BAA07938	BAA02633	D13370	87	APEX nuclease		2921.7	1942.2	-1.5	1.50432499
D50093	BAA08790	AAG21693	AY008282	59	Prion protein		32300.5	18687	-1.5	1.7285011
D86041	BAA18993	NP_036269	NM_012137	93	N-G,N-G-dimethylarginine dimethylaminohydrolase		4971.5	3409.6	-1.5	1.45808893
D87515	O09175	S65947	J03459	39	Aminopeptidase B		618.1	20	-1.5	30.905
D89069	BAA19007	NP_001748	NM_001757	85	Inducible carbonyl reductase		2396.6	1565.7	-1.5	1.53068915
D90401	BAA14397	XP_012353	XM_012353	75	Dihydrolipoamide succinyltransferase		3302.9	2255.3	-1.5	1.46450583
NM_031154	NP_112416	NP_000839	NM_000848	84	Rattus norvegicus glutathione S-transferase, mu type 3	E01415	4329.1	2880.8	-1.5	1.50274229
AK015150		XP_030759	XM_030759	89n	Mouse RIKEN; Human hypothetical protein	H33001	3967.4	2604.5	-1.5	1.52328662
H33086					Mus musculus, Similar to protein kinase, cAMP dependent regulatory, type I beta, clone MGC:18526 IMAGE:3674751		31376.4	21311.8	-1.5	1.47225481

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

H33093					EST(not recognised)		2003.4	1358.3	-1.5	1.4749319
NM_007798	NP_031824			No Human	Mus musculus cathepsin B	H33426	2944.6	1488.8	-1.5	1.9778345
J03481	AAA41099	XP_003584	XM_003584	89	Dihydropteridine reductase		8265.3	5667.4	-1.5	1.45839362
J04063	P11730	XP_044348	XM_044348	91	Rat calmodulin-dependent protein kinase II gamma subunit mRNA, complete cds		3558.4	2446.7	-1.5	1.45436711
J04503	AAA41917	NP_066283	NM_021003	98	Protein phosphatase 2c		1337.9	760.7	-1.5	1.75877481
K00750	AAA21711	NP_061820	NM_018947	91	chrome c nuclear-encoded mitochondrial gene and flanks	AI008815	6564.3	4376.3	-1.5	1.49996572
NM_031043	NP_112305	AAB09752	U31525	90n	Glycogenin	L01793	7189.3	4688.2	-1.5	1.53348833
L03294	Q06000	LIHUL	M15856	92	Lipoprotein lipase		1877	1287.6	-1.5	1.45775085
L07925	Q03386	Q12967	U14417	89	Ral guanine nucleotide dissociation stimulator		17631.9	11921.9	-1.5	1.4789505
L11025				No Human	Rat T-cell receptor alpha chain mRNA for RT1L haplotype		736.4	767	-1.5	0.9601043
L23148	AAA20403	BAA02989	D13890	88	Rattus norvegicus inhibitor of DNA-binding, splice variant Id1.25		1818.2	1190.5	-1.5	1.52725745
L24051	AAA41759	AAF19643	AF208502	91	Transcription factor		1083.3	733.5	-1.5	1.47689162
L26268	AAA85779	NP_001722	NM_001731	99	Anti-proliferative factor (BTG1)		2944.8	1977.4	-1.5	1.48922828
M15474	AAA21801	NP_000357	NM_000366	81	Alpha-tropomyosin gene, exon 11		7266.7	5337.1	-1.5	1.36154466
M15481	AAA41387	XP_052652	XM_052652	92	Insulin-like growth factor I (IGF-I)		4353.6	2830.7	-1.5	1.53799414
M18331	AAA41872	NP_005391	NM_005400	98	Protein kinase C epsilon		1817.3	2548.3	-1.5	0.71314209
M19357	AAA40988	NP_008822	NM_006891	76	Rat gamma-F-crystallin (gamma 4-1)		1039.3	686.1	-1.5	1.51479376
M24104	AAA42322	NP_055046	NM_014231	88	Vesicle associated membrane protein (VAMP-1)		8839.3	5852.8	-1.5	1.51026859
M27207		NP_000079	NM_000088	91n	Rattus norvegicus (clone pL6-3-1) alpha-1 type I collagen mRNA, 3' UTR		60274.4	41361.3	-1.5	1.45726561
M27467	AAA79270	Homology too low for human			Heart cytochrome oxidase subunit VIc (COX-VIc)		3759.4	2455.1	-1.5	1.53126148
M28648	AAA41672	XP_009351	XM_009351	63	Na,K-ATPase alpha-2 subunit mRNA, 5' end		3298.5	2260.1	-1.5	1.45856378
M34134	AAA42253	CAA27243	X03541	65	Alpha-tropomyosin (TMBr-2)		27548.1	12814.8	-1.5	2.14970971
M34331					Sequence intentionally withdrawn.		11124	7227.4	-1.5	1.53914271
M58758	AAA41962	NP_005168	NM_005177	91	Rat proton pump polypeptide		2973.9	2032.8	-1.5	1.4629575

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

M60322	AAA40721	NP_001619	NM_001628	85	Aldehyde reductase 1 (low Km aldose reductase) (5.8 kb PstI fragment, probably the functional gene)	15401.7	7231.2	-1.5	2.12989545
M60322	AAA40721	NP_001619	NM_001628	85	Aldehyde reductase 1 (low Km aldose reductase) (5.8 kb PstI fragment, probably the functional gene)	6728.4	4516	-1.5	1.48990257
M62388	AAA21087	CAA37339	X53251	100	Ubiquitin conjugating enzyme	2467.7	1665.2	-1.5	1.48192409
M65148	AAA42013	XP_027216	XM_027216	73	Rat RATF2	862.1	566.2	-1.5	1.52260685
M74439					UDP glucuronosyltransferase gene, complete cds	4653.6	4236.1	-1.5	1.09855764
M76426	AAC42062	I68600	M96860	93	Dipeptidylpeptidase 6	2799.8	1813.4	-1.5	1.54395059
M95591	Q02769	P37268	S76822	86	Farnesyl diphosphate farnesyl transferase 1	5203.8	3580.2	-1.5	1.45349422
S59892		XP_033168	XM_033168	92	La=autoantigen SS-B/La	2121.1	1379.5	-1.5	1.53758608
S61973	AAB20211	AAB94292	U44954	68	NMDA receptor glutamate-binding subunit	20271	14869.5	-1.5	1.36326037
S77900	AAB34127	XP_009501	XM_009501	96	myosin regulatory light chain isoform C; myosin RLC isoform C	3727.2	2448.2	-1.5	1.52366936
S81497	AAB36043	AAB60328	U08464	72	Lysosomal acid lipase=intracellular hydrolase	932.6	769	-1.5	1.21274382
S82649	AAB46783	AAH09924	BC009924	88	Narp=neuronal activity-regulated pentraxin	2014.5	3038.7	-1.5	0.66294797
S82911	AAB46839	NP_073207	NM_022716	95	rHox=rHox protein	1323.8	871.9	-1.5	1.51829338
S87522	AAB21778	NP_000886	NM_000895	87	Leukotriene A4 hydrolase	10206.2	6812.6	-1.5	1.49813581
S87522	AAB21778	NP_000886	NM_000895	87	Leukotriene A4 hydrolase	2800.4	5808.8	-1.5	0.48209613
U03390	AAA18951	NP_006089	NM_006098	99	Protein kinase C receptor	9701.4	7676.3	-1.5	1.26381199
U13176	AAA85101	NP_003330	NM_003339	100	ubc2e ubiquitin conjugating enzyme (E217kB	1224.7	967.1	-1.5	1.26636335
U17697	Q64654	AAB39951	U23942	93	Cytochrom P450 Lanosterol 14 alpha-demethylase	12716.8	8764.8	-1.5	1.45089449
U20796	AAA62508	BAA20088	D16815	86	Nuclear receptor Rev-ErbA-beta	944.4	620.1	-1.5	1.52298016
U27201	AAA75002	NP_000353	NM_000362	95	Tissue inhibitor of metalloproteinase 3 (TIMP-3)	2348.3	1844.8	-1.5	1.27292931
U31352	AAA91023	NP_002331	NM_002340	82	Oxidosqualene cyclase	2777.9	2159.5	-1.5	1.28636258
U32681	A57190	I38006	Z22971	40	Crp-ductin	7173.7	2763.7	-1.5	2.59568694

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

U34843	g1236114	g3551742	U27112	93	Rattus norvegicus cell cycle progression related D123 mRNA, complete cds (13 on d.s.)		2146	1667	-1.5	1.28734253
U34843	g1236114	g3551742	U27112	93	Rattus norvegicus cell cycle progression related D123 mRNA, complete cds (13 on d.s.)		1970.3	1352.1	-1.5	1.4572147
U38180	AAC61788	XP_036183	XM_036183		Reduced folate carrier membrane glycoprotein		1160.9	2524.8	-1.5	0.4597988
U39572	AAD10400	P42356	L36151	98	Phosphatidylinositol 4-kinase		3552	2445.8	-1.5	1.45228555
U45479	AAB60525	NP_003886	NM_003895	87	Synaptojanin		5939.4	4032.7	-1.5	1.47280978
U52102	AAB03280	NP_001304	NM_001313	89	rCRMP-1 mRNA		7624.6	5204.7	-1.5	1.46494515
U56242	AAB50063	AAC27038	AF055377	98	Transcription factor Maf2 mRNA		2299.6	1539.1	-1.5	1.49411994
U60977	AAC98706	NP_005794	NM_005803	83	Flotillin 1		14787.6	9884.9	-1.5	1.49597872
U67207	S74225	2211404A	U52912	87	Leptin receptor (fatty)		2319	1598.4	-1.5	1.45264345
U67995	AAB39620			No Human	Stearyl-CoA desaturase 2 mRNA		35115.6	22285.8	-1.5	1.57569394
U70476	AAC52898	NP_003036	NM_003045	81	Cationic amino acid transporter-1		1237.8	843.7	-1.5	1.46710916
U75411	AAB51477	CAA40956	X57819	53	Anti-idiotype immunoglobulin M light chain		1434	715.7	-1.5	2.00363281
NM_012656	NP_036788	NP_003109	NM_003118	83	SPARC	U75928	66640.7	45817.4	-1.5	1.45448454
U81492	AAC17704	NP_000579	NM_000588	29	Interleukin-3 beta		3164.6	500.2	-1.5	6.32666933
U87306	AAB57679	AAC67491	AF055634	62	Transmembrane receptor Unc5H2		7394.5	4906.5	-1.5	1.50708244
U90610	AAB50408	CAA12166	AJ224869	90	CXC chemokine receptor (CXCR4) mRNA		3294.6	2145.3	-1.5	1.53572927
U95727	AAB64094	NP_005871	NM_005880	86	DnaJ homolog 2 mRNA		1323.9	1051.2	-1.5	1.25941781
U97142	Q62997	P56159	U59486	92	Glial cell line-derived neurotrophic factor receptor alpha (42 on d.s.)		2370.7	1598.8	-1.5	1.4827998
V01216	P02764	P02763	X02544	51	Rat messenger encoding alpha-1-acid glycoprotein		782.4	524.8	-1.5	1.49085366
X04139	CAA27756	NP_002729	NM_002738	100	Protein kinase C		2570	1727.3	-1.5	1.48787124
X05341	CAA28952	XP_030051	XM_030051	87	3-oxoacyl-CoA thiolase		5255.4	3523.3	-1.5	1.49161298
X06889	3RABA	P20336	M28210	98	Ras-related small GTP binding protein 3A		12454	8347.9	-1.5	1.49187221
X07551					Sequence intentionally withdrawn.		7345.9	4994.9	-1.5	1.47068009
X07648	CAA30488	XP_047792	XM_047792	81	Amyloidogenic glycoprotein (rAG), cognate of human A4 amyloid precursor protein		21040.8	14125.1	-1.5	1.48960361
X08056	CAA30845	NP_000147	NM_000156	85	Guanidinoacetate methyltransferase		4795.9	2620.9	-1.5	1.8298676

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

X12367	CAA30928	CAB37833	Y00483	86	Glutathione peroxidase I		11490.9	7541	-1.5	1.52378995
X12535	CAA31053	XP_031588	XM_031588	99	Ras-related protein p23		4338	2987.6	-1.5	1.45200161
X13722	CAA32001	AAF24515	AF217403	73	LDL-receptor precursor		2079.8	1380.5	-1.5	1.5065556
X14848					Mitochondrial genome		1804.9	1241.8	-1.5	1.45345466
X15096	CAA33199	NP_000993	NM_001002	94	Acidic ribosomal phosphoprotein P0		66106.6	45362.4	-1.5	1.45729944
NM_013059	NP_037191	XP_001826	XM_001826	91	Tissue-nonspecific ALP alkaline phosphatase	X16038	1105.4	745.7	-1.5	1.48236556
X16703	CAA34674	NP_000603	NM_000612	57	Insulin-like growth factor II		585.9	395.9	-1.5	1.47991917
X16933	CAA34808	AAA35781	M94630	81	hnRNP C protein		1017.6	699.3	-1.5	1.45516946
X51615		XP_007169	XM_007169	86	Connexin protein Cx26		1462.3	957.6	-1.5	1.52704678
X54081	CAA38018	NP_001852	NM_001861	79	RCO4-1 gene for cytochrome c oxidase subunit IV		25191.1	16905.8	-1.5	1.49008624
X54617	CAA38437	XP_041677	XM_041677	100	RLC-A gene for myosin regulatory light chain		4714.5	3154.9	-1.5	1.49434213
X55298	CAB56805	XP_009642	XM_009642	88	Rat ribophorin II mRNA		4849.6	3275.1	-1.5	1.48074868
X62875		XP_043244	XM_043244	89n	High Mobility Group Protein I (Y), 3' UTR		15175.9	10113.2	-1.5	1.50060317
X73653	CAA52020	NP_002084	NM_002093	95	Tau protein kinase I		1165.1	352.9	-1.5	3.30150184
X76489	CAA54027	NP_001760	NM_001769	79	CD9 mRNA for cell surface glycoprotein		32675.3	22225.6	-1.5	1.47016503
X76988	CAA54293	NP_008858	NM_006927	93	Gal beta 1,3-GalNAc alpha-2,3-sialyltransferase		882.1	592.3	-1.5	1.48927908
X77934	CAA54906	NP_001633	NM_001642	79	Amyloid precursor-like protein 2		5226.8	3456.9	-1.5	1.51199051
X80290	CAA56564	XP_012740	XM_012740	80	Adenylate cyclase activating peptide		2240.1	2569.3	-1.5	0.87187172
X82152	CAA57648	XP_001782	XM_001782	81	Fibromodulin		577.5	388.3	-1.5	1.48725212
X84039	CAA58858	NP_002336	NM_002345	80	Lumican		10431.1	6746.6	-1.5	1.54612694
Y17606	CAA76804	XP_009523	XM_009523	78	Potassium channel, alpha subunit (Kv9.1)		3135.5	1068.9	-1.5	2.93338947
Z12298	CAA78170	NP_001911	NM_001920	74	Dermatan sulfate proteoglycan-II (decorin)		24967.7	16776.9	-1.5	1.48821892
Z17319	CAA78967	AAH01904	BC001904	93	Phosphoglyceromutase		1978.1	1292	-1.5	1.52948916
Z29072	CAA82313			Human too low	Mucin		626.4	366.4	-1.5	1.70960699
AK005159	BAB23850	AF125533	AAF17227	84	NADH-cytochrome b5 reductase isoform	AA685876	8773.1	6494.3	-1.4	1.35089232
AK003201	BAB22637	XP_006307	XM_006307	81n	Mouse RIKEN; Human hypothetical protein	AA799442	970.1	680.2	-1.4	1.42619818

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

NM_017340	NP_059036	AAH08767	BC008767			AA799489				
				85	Rattus norvegicus acyl-coA oxidase		9095.5	6319.9	-1.4	1.43918416
AA799511		AAC09039	AC004520	97n	Human Clone		699.5	517.1	-1.4	1.35273641
AA799515					EST(not recognised)		4536.6	6190.6	-1.4	0.73282073
BC011510	AAH11510	XP_009884	XM_009884		Mus musculus, Similar to small	AA799526				
				91n	nuclear ribonucleoprotein D3		2729.3	1892.5	-1.4	1.44216645
AF250133		XP_036785	XM_036785		Mus musculus splicing factor Sc35	AA799538				
					(Pr264) mRNA, 3'UTR, alternatively					
				93n	spliced		2336.8	1655.5	-1.4	1.4115373
AA799581		Q93075	D86972		ESTs, Moderately similar to					
					PUTATIVE DEOXYRIBONUCLEASE					
				89	KIAA0218 [H.sapiens]		1332	2691.3	-1.4	0.4949281
NM_019386	NP_062269	XP_035350	XM_035350		Mus musculus cysteine and histidine-	AA799721				
				93n	rich protein		1005.4	722.9	-1.4	1.39078711
X14181	CAA32385	NP_000971	NM_000980			AA799899				
				99	Rat mRNA for ribosomal protein L18a		46447.2	34176.4	-1.4	1.35904308
NM_025277	NP_079553				Mus musculus guanine nucleotide	AA799996				
				Human	binding protein (G protein), gamma					
				too low	10		4491.4	2138.1	-1.4	2.10065011
AA800034					EST (not recognized)		7527.4	5385.1	-1.4	1.39781991
U68134	AAC52608	XP_040847	XM_040847		Mus musculus poly(A) polymerase VI	AA800296				
				95n	mRNA		868.5	699.9	-1.4	1.24089156
AA800637	BAB27481		AF147398		Homo sapiens full length insert cDNA					
				97n	clone		1053	772.5	-1.4	1.3631068
AA800749					EST(not recognised)		5240.5	3799	-1.4	1.37944196
AJ010709	CAA09309	NP_000344	NM_000353		Rattus norvegicus gene encoding	AA800750				
				90	tyrosine aminotransferase		3118.3	2225.4	-1.4	1.40123124
AA800794					Mus musculus 10 day old male					
					pancreas cDNA, RIKEN		1009.8	1427.1	-1.4	0.70758882
AA800803					EST (not recognized)		4274.5	5141.2	-1.4	0.83142068
AK005487	BAB24073				Mouse RIKEN	AA800822	1912.1	1393.3	-1.4	1.37235341
AF357008	AAK97375	NP_005567	NM_005576	85n	Mus musculus lysyl oxidase-like 1	AA800844	4127.8	3056.4	-1.4	1.35054312
U90556	AAB50246	CAC14588	Y14436		Rattus norvegicus phosphatidate	AA818593				
				83	phosphohydrolase type 2		6929.8	4928.1	-1.4	1.40618088
AF090347	AAG24489	XP_005557	XM_005557		Rattus norvegicus putative G-protein	AA848831				
				95	coupled receptor GPCR91		3884.5	2731.2	-1.4	1.41494581
M27905	AAA41504	AAA85655	U14967		Rattus norvegicus ribosomal protein	AA849648				
				98	L21 mRNA		1359.9	1005.8	-1.4	1.35205806
U75411	AAB51477	CAA40956	X57819		Rattus norvegicus anti-idiotype	AA850138				
				53	immunoglobulin M light chain		4913.1	3600.1	-1.4	1.36471209

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

AF148511	AAD39516	NP_006858	NM_006867	84(mus)	Mus musculus hermes mRNA	AA859519	1349.6	762.8	-1.4	1.76927111
AA859672		XP_040014	XM_040014	86n	Homo sapiens hypothetical protein MGC3103		3302.4	2348.7	-1.4	1.40605441
AA859705		XP_046017	XM_046017	92	Homo sapiens hypothetical protein DKFZp761G2113		3711.2	2724.1	-1.4	1.36235821
AA859750					EST (not recognized)		1392.4	707.6	-1.4	1.96777841
AA859832					Mus musculus 18 days embryo cDNA, RIKEN		1330.8	617.1	-1.4	2.15653865
AA859878					EST (not recognized)		7709.1	4852.6	-1.4	1.58865351
AK003842	BAB23031				Mouse RIKEN	AA866371	4865.5	4816.4	-1.4	1.01019434
NM_030261	NP_084537			No Human	Mouse Hypothetical Protein	AA874873	1172	861.8	-1.4	1.3599443
AA874926					Homo sapiens mRNA; cDNA DKFZp434M1616		4178	2916.5	-1.4	1.432539
AA874927					EST(not recognised)		2852.1	2001.7	-1.4	1.42483889
AA875017					EST (not recognized)		12515	5752	-1.4	2.17576495
AA875127	BAB26250	CAC10401	AJ297710	92n	CDC2L5 protein kinase (Rat EST; mouse hypothetical protein)		1550.6	1139.9	-1.4	1.36029476
AA875268		XP_027422	XM_027422	96	ESTs, Highly similar to NUKM_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE 20 KDA SUBUNIT PRECURSOR [H.sapiens]		7181.2	5127.6	-1.4	1.40049926
AA875425					Human DNA sequence from clone RP5-1169J3		3080.8	2262.2	-1.4	1.36186014
AA875496					Mus musculus 10 days neonate cerebellum cDNA, RIKEN		504.3	373.1	-1.4	1.35164835
NM_019128	NP_062001	NP_116116	NM_032727	71	Internexin, alpha	AA875659	1624.3	1161.7	-1.4	1.39820952
NM_012656	NP_036788	NP_003109	NM_003118	83	Secreted acidic cystein-rich glycoprotein	AA891204	9944.7	7433	-1.4	1.33791201
AA891207					EST (not recognized)		7588.1	5457.3	-1.4	1.39044949
AK018016	BAB31038	XP_035638	XM_035638	88n	Mouse RIKEN; Human hypothetical protein	AA891209	2133.9	1473.9	-1.4	1.44779157
AA891727		XP_042640	XM_042640	92n	EST (hypothetical protein)		2098.8	1511.3	-1.4	1.38741481
NM_019768	NP_062742	XP_034440	XM_034440	91n	Mus musculus MORF-related gene X	AA891789	8200.5	5974.1	-1.4	1.37267538
AA891796					Mus musculus ES cells cDNA, RIKEN		8750	6110.2	-1.4	1.43203168
NM_021540	NP_067515	XP_003972	XM_003972	89n	Mus musculus g1-related zinc finger protein	AA891810	2537.4	1857.7	-1.4	1.36588254

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

NM_021640	NP_067515	XP_003972	XM_003972	89n	Mus musculus g1-related zinc finger protein	AA891810	1410.2	749.2	-1.4	1.88227443
AA891812	S54147	S18207	X58141	94	ESTs, Highly similar to S54147 alpha adducin - rat [R.norvegicus]		4609.2	3358.4	-1.4	1.37243926
NM_022545	NP_071990	XP_008138	XM_008138	92	Phosphoribosylpyrophosphate synthetase-associated protein	AA891871	3143.7	2205.2	-1.4	1.42558498
NM_010413	NP_034543	XP_028575	XM_028575	86n	Mus musculus histone deacetylase 6	AA892036	2188.5	1514.9	-1.4	1.44464981
AA892049					EST (not recognized)		2761.4	2005.2	-1.4	1.37711949
AA892083					EST(not recognised)		2783.6	1960	-1.4	1.42020408
AK013082					Mouse RIKEN with low homolgy to MAD4 homolog (Homo sapiens)	AA892154	2509.9	1085.2	-1.4	2.31284556
AA892425					Mus musculus 11 days embryo cDNA, RIKEN		1152.7	827.6	-1.4	1.39282262
AA892486	A36690	A32609	Y00839	79	ESTs, Weakly similar to A36690 sucrose alpha-glucosidase [R.norvegicus]		10219.9	7225.4	-1.4	1.41444072
AA892496		XP_041304	XM_041304	93n	Weak homology with Homo sapiens chimerin (chimaerin) 2 (CHN2)		1867.8	1313.8	-1.4	1.42167758
AA892522					EST (not recognized)		1197.9	847	-1.4	1.41428571
AA892554		XP_032936	XM_032936	86n	Homo sapiens similar to RAS-GTPASE-ACTIVATING PROTEIN BINDING PROTEIN 2	AA892554	2094.5	1547.2	-1.4	1.35373578
Z34922	CAA84402	NP_001354	NM_001363	81	R.norvegicus mRNA for nucleolar protein NAP57	AA892562	2793.6	2026.2	-1.4	1.37873853
NM_025363	NP_079639	AAH08467	BC008467	90n	Mouse RIKEN; Human hypothetical protein	AA892572	3071.6	2183.9	-1.4	1.40847468
AA892635	TVRTRH	TVHUC4	M31470	99	Ras-like protein		4837.3	2479	-1.4	1.95131101
X74125	CAA52225	NP_004126	NM_004135	86	R.norvegicus mRNA for NAD+-isocitrate dehydrogenase, gamma subunit	AA892808	2539.7	1876	-1.4	1.35378465
NM_011962	NP_036092	NP_001075	NM_001084	87n	Mus musculus procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	AA892859	5038.5	3588.3	-1.4	1.40414681
AA892888					EST (not recognized)		4324	5673.3	-1.4	0.76216664
NM_009386	NP_033412	XP_007585	XM_007585	88n	Mus musculus tight junction protein 1	AA892918	3118.7	1881.6	-1.4	1.65747236
NM_008942	NP_032968	XP_032201	XM_032201	90n	Mus musculus puromycin-sensitive aminopeptidase	AA893065	7118.1	4996.3	-1.4	1.42467426

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

AA893183		XP_017866	XM_017866	84n	Homo sapiens hypothetical protein FLJ12529		2354.5	1646.6	-1.4	1.42991619
NM_007457	NP_031483	XP_051246	XM_051246	86n	Mus musculus adaptor protein complex AP-1, sigma 1	AA893202	5046.5	3498.8	-1.4	1.44235166
AA893230					Mus musculus adult male tongue cDNA, RIKEN		959.3	702.7	-1.4	1.36516294
AA893353					ESTs, Weakly similar to T15946 hypothetical protein F01F1.9 [C.elegans]		6094.5	5152.4	-1.4	1.18284683
NM_013160	NP_037292	XP_045326	XM_045326	73	Rattus norvegicus Max interacting protein 1	AA893611	5276.1	4054	-1.4	1.30145535
BC004091		Homology too low for Humans			Mouse Clone	AA893643	7618.1	5616.7	-1.4	1.35633023
NM_019435	NP_062308	AAH10665	BC010665	86n	Mus musculus neuronal protein 15.6	AA893690	2481.3	2045.5	-1.4	1.21305304
AF229439	AAF91258	XP_037147	XM_037147	85n	Mus musculus zinc finger protein 289	AA893741	4313.4	2980.1	-1.4	1.44740109
AK010212					Mouse RIKEN	AA893743	2821.7	2044.2	-1.4	1.38034439
AA893869					ESTs, Weakly similar to T16084 hypothetical protein F16H11.1 [C.elegans]		1938.9	1886.5	-1.4	1.02777631
D32249	BAA06979	XP_003693	XM_003693	78	Rattus norvegicus mRNA for neurodegeneration associated protein 1	AA894089	5591.4	3972.5	-1.4	1.40752675
AF305619	AAL09361	NP_006550	NM_006559	63	Nuclear RNA binding protein Sam68	AA894160	1720.2	1244.9	-1.4	1.38179773
AA899253	P36198	P50458	U11701	92	Myristoylated alanine-rich protein kinase C substrate		6265.5	4636	-1.4	1.35148835
AA899320		XP_029314	XM_029314	82n	Homo sapiens NADH dehydrogenase		7508.7	7661.8	-1.4	0.98001775
NM_012974	NP_037106	CAA56130	X79683	81	Rattus norvegicus Laminin chain beta 2	AA900848	3101.4	2250.1	-1.4	1.37833874
L78075	AAB40051	XP_017159	XM_017159	95n	Mus musculus Cdc42 gene	AA925473	19747.9	13675.3	-1.4	1.44405607
X53565	CAA37637	AAC39542	AF027516	44	Rat mRNA for trans-Golgi network integral membrane protein TGN38	AA926292	3227.2	2359.7	-1.4	1.36763148
AK013911	BAB29050	NP_055148	NM_014333	90n	Homo sapiens immunoglobulin superfamily, member 4; Mouse RIKEN	AA933181	921.7	677.8	-1.4	1.35984066
NM_024152	NP_077066	NP_001654	NM_001663	100	Rattus norvegicus ADP-ribosylation factor 6	AA944324	1562	1104	-1.4	1.41485507

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

X75207	CAA53020	AAH00076	BC000076	83	CCND1 mRNA for cyclin D1	AA957218	1829.7	2896	-1.4	0.63180249
D00636	BAA00530	NP_000389	NM_000398	83	NADH-cytochrome b5 reductase	AA963839	6815.5	5037.4	-1.4	1.35297971
AB000280	g2208839	Q16348	S78203	23	Peptide/histidine transporter		1812.2	1316	-1.4	1.37705167
AB004096	BAA20354	Q16850	U23942	89	Lanosterol 14-demethylase	AA963449	4884	3450.4	-1.4	1.41548806
AB006914	BAA22191	NP_004231	NM_004240	78	Rattus norvegicus mRNA for salt-tolerant protein		1555.4	1987.1	-1.4	0.78274873
AB010466	BAA28954	NP_001162	NM_001171	73	Rattus norvegicus mRNA for multidrug resistance-associated protein (MRP)-like protein-1		1408.8	1035.5	-1.4	1.35857074
AB011679	BAA32736	AAC28642	AF070561	95	Class I beta-tubulin		1505.2	1104.8	-1.4	1.36241854
AB015432	BAA33035	NP_003477	NM_003486	83	LAT1 (L-type amino acid transporter 1)		10494.3	4637.2	-1.4	2.26306823
AB015946	A25113	UBHUG	M61764	98	Rattus norvegicus mRNA for tubulin, complete cds		3704.8	2084.6	-1.4	1.77722345
AB016160	Q9Z0U4	Q9UBS5	AJ225028	97	Gamma-aminobutyric acid (GABA) B receptor, 1		4928.3	3630.5	-1.4	1.35747142
AB016160	Q9Z0U4	Q9UBS5	AJ225028	97	Gamma-aminobutyric acid (GABA) B receptor, 1		4751.1	3460.6	-1.4	1.37291221
AB016800	BAA34306	XP_006067	XM_006067	82	7-dehydrocholesterol reductase		5720	2797.7	-1.4	2.04453658
AB017170	BAA35187	BAA35184	AB017167	96	Rattus norvegicus mRNA for Slit-1 protein, partial cds		3105.6	2222.8	-1.4	1.39715674
AF008439	AAC53319	NP_000608	NM_000617	78	natural resistance-associated macrophage protein 2		1808.1	1322.6	-1.4	1.36707999
AF008554	AAB63294	AAB18374	U42349	71	Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds		617.4	579.4	-1.4	1.06558509
AF001282	AAB65640	NP_000185	NM_000194	95	Hypoxanthine guanine phosphoribosyl transferase	AF009656	2595.9	1814.3	-1.4	1.43079976
AF012714	AAC53453	XP_005866	XM_005866	84	Hepatic multiple inositol polyphosphate phosphatase		2222.5	1301.6	-1.4	1.70751383
AF013144	AAB94858	NP_004410	NM_004419	87	Rattus norvegicus MAP-kinase phosphatase (cpg21) mRNA, complete cds		606.4	842.6	-1.4	0.71967719
AF016178	AAC53325	Homology too low for Humans			Putative pheromone receptor (Go-VN1)		1422	584.3	-1.4	2.43368133
AF020211	AAB71236	NP_005681	NM_005690	83	DLP1 splice variant 1		2024.4	1416.7	-1.4	1.42895461
AF021923	AAC19405	XP_048312	XM_048312	84	Potassium-dependent sodium-calcium exchanger		2659.8	1938.7	-1.4	1.37195028

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

M18416	AAA61927	XP_033545	XM_033545	89n	Rattus norvegicus nerve growth factor induced factor A	AF023087	4680.3	3371	-1.4	1.38840107
AF027954	AAB87418	NP_055019	NM_014204	98	Bcl-2-related ovarian killer protein (Bok)		3453.7	2462.8	-1.4	1.40234692
AF030558	AAC40202	NP_003550	NM_003559	56	Phosphatidylinositol 5-phosphate 4-kinase gamma		1882.5	1360.5	-1.4	1.38368247
AF034237					EST also named DD6A4-1 mRNA		5598.5	3562.5	-1.4	1.57150877
AF034582	AAD01990	BAA74928	AB020712	79	Vesicle associated protein (VAP1)		2517.4	1774.8	-1.4	1.41841334
AF036548	AAC68839	NP_054778	NM_014059	74	RGC-32		1994.8	1452.7	-1.4	1.37316721
AF048828	AAD02476	NP_003365	NM_003374	93	Rattus norvegicus voltage dependent anion channel (RVDAC1)		1267.4	896.8	-1.4	1.4132471
AF051425	AAC05574	NP_008946	NM_007015	88	Chondromodulin-1 (Chm-1)		8151.4	7394.2	-1.4	1.10240459
AF058795	AAC63994	AAD45867	AF099033	95	GABA-B receptor gb2		6797.1	4842.4	-1.4	1.40366347
AF064868	AAC63267	NP_065887	NM_020836	79	Brain-enriched guanylate kinase-associated protein 1		1840	1285.6	-1.4	1.43123833
AF067795	AAC79427	NP_001319	NM_001328	90	BFA-dependent ADP-ribosylation substrate		7144.1	5201.1	-1.4	1.37357482
AF074609	AAC33332		No Human		MHC class I antigen (RT1.EC3) gene		11693.7	8256.4	-1.4	1.41631946
AF076183	AAC31815	XP_008499	XM_008499	90	Cytosolic sorting protein PACS-1a		3227.3	2359.4	-1.4	1.36784776
AF079162	AAC99398	NP_000255	NM_000264	92	Rattus norvegicus patched (ptc) mRNA, partial cds		3093.1	2211	-1.4	1.39895975
AF083269	O88656	O15143	AF006084	96	Actin-related protein complex 1b (14 on d.s.)		3358.4	2462.8	-1.4	1.36365113
AF087431	AAC36477	XP_035229	XM_035229	78	Glycoprotein processing glucosidase I		2555.8	1771.6	-1.4	1.44265071
AF087437		NP_074036	NM_022845	89n	PEBP2 beta mRNA, 3' UTR		21526.8	15828.6	-1.4	1.35999394
AF087697	AAC78485	XP_008354	XM_008354	97	dlg 3		4211	2118.5	-1.4	1.98772717
AF087943	AAC35371	NP_000582	NM_000591	64	CD14 mRNA		1434.1	1037.7	-1.4	1.38199865
AF093139	AAC63367	XP_043248	XM_043248	84	Rattus norvegicus tip associating protein (TAP) mRNA		3212.3	2278.8	-1.4	1.40964543
AF095927	AAC97497	NP_110395	NM_030768	87	Protein phosphatase 2C mRNA		1327.7	970.4	-1.4	1.36819868
AF097723	AAC72384	NP_057218	NM_016134	83	Rattus norvegicus hematopoietic lineage switch 2 related protein		3324.1	1932.3	-1.4	1.72028153
AI007824	CAA49904	AAB18264	U74324	91	R. norvegicus mRNA for Mss4 protein		164159.2	113399.6	-1.4	1.4476171
AI007824	CAA49904	AAB18264	U74324	91	R. norvegicus mRNA for Mss4 protein		55098	40702.7	-1.4	1.35366941

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

S45392	AAB23369	NP_031381	NM_007355	85	Heat shock protein 90	AI008074	15494.1	11103.4	-1.4	1.39543743
AI009147		CAB96537	AJ249980	86	EST (human hypothetical protein)		3461.3	1687.6	-1.4	2.0510192
NM_031051	NP_112313	NP_002406	NM_002415	95	Rattus norvegicus macrophage migration inhibitory factor (Mif)	AI009801	5403.7	4569.3	-1.4	1.18261003
AI012275	g310100	g3294180	Z99129	40	Developmentally regulated protein mRNA		958.1	936.9	-1.4	1.02262782
NM_013224	NP_037356	XP_015318	XM_015318	100	Rattus norvegicus ribosomal protein S26	AI014087	20479.9	14848.3	-1.4	1.37927574
U30789					Rattus norvegicus clone N27	AI014169	10327.2	7535.5	-1.4	1.37047309
NM_022297	NP_071633	NP_036269	NM_012137	93	Rattus norvegicus NG,NG dimethylarginine dimethylaminohydrolase	AI058941	1091.1	1790.1	-1.4	0.60951902
AI059291	P12368	P13861	X14968	87	Protein kinase, cAMP dependent regulatory, type II alpha		3039.9	2171	-1.4	1.40023031
NM_012959	NP_037091	NP_005255	NM_005264	92	Rattus norvegicus Glial cell line-derived neurotrophic factor receptor alpha	AI070721	2638.2	1898.7	-1.4	1.38947701
NM_012903	NP_037035	NP_006296	NM_006305	81	Rattus norvegicus Acid nuclear phosphoprotein 32 (leucine rich)	AI070967	3330.1	2424.6	-1.4	1.37346366
AK017379					Mouse RIKEN	AI103874	2273	1585.7	-1.4	1.43343634
M24542	AAA42051	NP_005994	NM_006003	85	Rat Rieske iron-sulfur protein	AI103911	6932.2	4832.2	-1.4	1.43458466
AF012714	AAC53453	XP_005866	XM_005866	84	Hepatic multiple inositol polyphosphate phosphatase	AI111401	1161.2	846	-1.4	1.37257683
NM_012637	NP_036769	NP_002818	NM_002827	81	Rattus norvegicus Protein-tyrosine phosphatase	AI113289	1076.8	772.1	-1.4	1.394638
NM_031020	NP_112282	XP_043351	XM_043351	94	p38 mitogen activated protein kinase (Mapk14)	AI137862	6631.6	3548	-1.4	1.86910936
NM_031719	NP_113907	NP_001284	NM_001293	78	Rattus norvegicus chloride channel current inducer	AI169005	1468.3	1041	-1.4	1.4104707
NM_031616	NP_113804	AAD09746	AF065391	54	Rattus norvegicus zinc finger protein 265	AI170608	2874.1	2059.5	-1.4	1.3955329
M60523	AAA37818	NP_002158	NM_002167	83	Mouse helix-loop-helix protein (Id related)	AI171268	5236.5	3724.1	-1.4	1.40611154
J01436	AAA99907			No Human	Cytochrome B gene	AI171355	73530.7	53883	-1.4	1.36463634
M26594	AAA41563	AAB01380	L34035	88	Rattus norvegicus malic enzyme	AI171506	2557.8	1886.4	-1.4	1.35591603
AI175935					Mus musculus adult male cecum cDNA, RIKEN		1844.9	1316	-1.4	1.4018997
BC004671	AAH04671	NP_000792	NM_000801	97(mus)	Mus musculus, FK506 binding protein 1a	AI176170	18902.6	13099.4	-1.4	1.44301266

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

BC012522	AAH12522	AAH11890	BC011890		Mouse RIKEN; Homo sapiens, Similar to electron-transferring-flavoprotein dehydrogenase	AI176422	1830.7	454.9	-1.4	4.02440097
				94n						
AI176480					Rattus norvegicus genes for 18S, 5.8S, and 28S ribosomal RNAs		4677.5	4755.6	-1.4	0.98359794
AF013598	AAB69328	NP_004760	NM_004769		Rattus norvegicus proton gated	AI179632				
				80	cation channel DRASIC mRNA		7049.9	5096.9	-1.4	1.38317409
AI230130	g2648049	AAD40239	AF144748	82	Testicular ecto-ATPase		3754.1	2627.2	-1.4	1.42893575
NM_013060	NP_037192	XP_002273	XM_002273		Rattus norvegicus inhibitor of DNA binding 2, dominant negative helix-loop-helix protein (Id2)	AI230256				
				97			2840.2	1973.4	-1.4	1.43924192
AK012933		XP_039754	XM_039754			AI230406				
				95n	Mouse RIKEN;Homo sapiens RAB10		10452.5	8898.5	-1.4	1.17463617
U20525	AAA62507	NP_003286	NM_003295		Rattus norvegicus lens epithelial	AI230748				
				95	protein		77943.8	47163.8	-1.4	1.65261917
NM_017322	NP_059018	AAA56831	L31951		Rattus norvegicus stress activated	AI231354				
				92	protein kinase alpha II		521.6	20	-1.4	26.08
NM_016988	NP_058684	AAH03160	BC003160		Rattus norvegicus Acid phosphatase	AI234950				
				86	2, lysozymal		1698.4	1197.2	-1.4	1.4186435
AI235707					Double cDNA (calnexin and p62 dynactin)		3286.9	2654.9	-1.4	1.2380504
NM_017182	NP_058878	XP_003835	XM_003835		Rattus norvegicus H2A histone	AI237016				
				89	family, member Y		3068.5	3494.4	-1.4	0.87811828
AK003762		XP_051511	XM_051511		Mouse RIKEN; Human hypothetical	AI237378				
				93n	protein		10656.6	7811.1	-1.4	1.36428928
AI639101					EST (not recognized)		1130.6	93.2	-1.4	12.1309013
AI639157	AAB71495	NP_005214	NM_005223	71	Deoxyribonuclease I (DNaseI) ??		4397.4	3039.4	-1.4	1.44679871
AI639176					EST (not recognized)		796.2	582.6	-1.4	1.36663234
AI639204					EST (not recognized)		905.6	364.7	-1.4	2.48313682
AI639207					EST (not recognized)		5992.1	4371.9	-1.4	1.37059402
AI639236					EST (not recognized)		1164.3	836.8	-1.4	1.39137189
AI639239					EST (not recognized)		702.9	504.5	-1.4	1.39326065
AI639345					EST (not recognized)		1498.5	705.8	-1.4	2.1231227
AI639461					EST (not recognized)		1714.1	1246.4	-1.4	1.37524069
AI639501		NP_113630	NM_031442		Hypothetical protein					
				88n	DKFZp761J17121 [Homo sapiens].		4894.8	2746.8	-1.4	1.78200087
AJ000485	CAA04123	XP_054486	XM_054486	78	CLIP-115		3387.9	4017.1	-1.4	0.84336959
AJ001290	CAA04650	XP_009743	XM_009743		Sodium myo-inositol transporter					
				93	(SMIT)		2395.9	1438.5	-1.4	1.6655544

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

AJ007422	CAA07496	NP_006860	NM_006869	94	IP4/PIP3 binding protein		4364	3115	-1.4	1.40096308
D00569	BAA00446	NP_001350	NM_001359	81	2,4-dienoyl-CoA reductase precursor		910.5	1065.2	-1.4	0.85476906
D13124	BAA02426	NP_005167	NM_005176	75	P2 mRNA for ATP synthase subunit c		17227	12011.3	-1.4	1.43423276
D13127	Q06647	CAA58219	X83218	81	Rattus norvegicus mRNA for oligomycin sensitivity conferring protein, complete cds		14754.5	16106	-1.4	0.91608717
D13309	BAA02569	AAA35750	M24070	59	DNA-binding protein B		9538.2	6835.3	-1.4	1.39543253
D14421	BAA03313	NP_004567	NM_004576	100	b isotype of B regulatory subunit of protein phosphatase 2A		1704.5	1200.2	-1.4	1.42017997
D21800	BAA04824	NP_002786	NM_002795	98	Proteasome subunit RC10-II		9685.8	6980.8	-1.4	1.3874914
D26073	BAA05068	XP_008138	XM_008138	92	Phosphoribosylpyrophosphate synthetase-associated protein (39 kDa)	AA891871	3405.7	2434.2	-1.4	1.39910443
D28512	BAA05870	NP_115674	NM_032298	71	Synaptotagmin III		3468.3	2445.6	-1.4	1.41817959
D29683	BAA08152	XP_033687	XM_033687	90	Endothelin-converting enzyme	AA956930	5383.1	3919.5	-1.4	1.37341498
D29960	BAA06227	NP_001876	NM_001885	46	AlphaB crystallin-related protein	AI103838	618.3	1192.1	-1.4	0.51866454
D70817	BAA11097	NP_006642	NM_006651	56	Synaphin 2		9368.6	8435.4	-1.4	1.11062902
D83349	BAA11895	XP_008821	XM_008821	54	Short type PB-cadherin		16455.2	11964.7	-1.4	1.37531238
D83538	BAA19614	NP_002641	NM_002650	98	230kDa phosphatidylinositol 4-kinase		4756.1	3324.2	-1.4	1.43075026
D83948	BAA12144	AAH04181	BC004181	81	S1-1 protein		2535	1248.2	-1.4	2.03092453
D85435	BAA36277	AAK97528	AF408198	71	Protein kinase C delta-binding protein		10175.6	7031.9	-1.4	1.44706267
D86297	BAA13063	NP_001686	NM_001695	95	Erythroid-specific delta-aminolevulinate synthase		5939.4	4223.8	-1.4	1.40617453
D87336	BAA13333	NP_000377	NM_000386	93	Bleomycin hydrolase		4306.6	1615.2	-1.4	2.6662952
H31313					EST(not recognised)		6500.3	3704.8	-1.4	1.75456165
AC091616				No Human	Rat clone	H31323	832.1	776.7	-1.4	1.07132741
NM_025927	NP_080203	NP_115727	NM_032351	82n	Mus musculus mitochondrial ribosomal protein L45	H31489	3349.2	2393	-1.4	1.39958211
H31648					EST (not recognized)		1693.8	1236.9	-1.4	1.36939122
H31722					EST (not recognized)		2997.1	2109	-1.4	1.42110005
H31802	S12207		No human		EST, Moderately similar to S12207 hypothetical protein [M.musculus]		1742.1	1222.4	-1.4	1.42514725
AK004235	BAB23231				Mouse RIKEN	H31847	7466.9	5342.4	-1.4	1.39766771
H31859					EST (not recognized)		675.1	489.7	-1.4	1.37859914

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

H33459					Mus musculus adult male small intestine cDNA, RIKEN		6478.6	4738.1	-1.4	1.36734134
AF333986	AAK29401	AAG25715	AF309387	93	Nucleolar protein C7C	H33461	3259.9	2388.9	-1.4	1.36460296
H33619					EST (not recognized)	H33619	742.7	520.9	-1.4	1.4258015
J01435					Mitochondrial cytochrome oxidase subunits I,II, III		272027.3	200600	-1.4	1.3560683
J03637	AAA40713	AAH04370	BC004370	81	Aldehyde dehydrogenase		2274.8	1031.2	-1.4	2.20597362
J04147	AAA41089	NP_000367	NM_000376	83	1,25-dihydroxyvitamin D-3 receptor		3798.5	4223.2	-1.4	0.89943645
J05022	DIRTR1	Q9Y2J8	AB030176	93	Peptidyl arginine deiminase, type II		6417.5	3528.1	-1.4	1.81896772
L00191	AAA41166	NP_002017	NM_002026	72	Rat fibronectin		3431.7	3370.8	-1.4	1.01806693
NM_031043	NP_112305	AAB09752	U31525	90n	Glycogenin	L01793	4181.2	2339.8	-1.4	1.78699034
L02530	AAA41172	NP_001457	NM_001466	94	Rattus norvegicus Drosophila polarity gene (frizzled) homologue		3292	1918.9	-1.4	1.71556621
L02615	AAA40867	NP_006814	NM_006823	97	cAMP-dependent protein kinase inhibitor (PKI)		1849.4	1309.2	-1.4	1.41261839
L04485	AAA41571	NP_002746	NM_002755	90	MAP kinase kinase mRNA		5954.3	4285.1	-1.4	1.38953583
L04739	AAA50878	AAA36000	M95542	56	Plasma membrane calcium ATPase.		2636.7	1602.6	-1.4	1.64526395
L05435	AAA42188	NP_055664	NM_014849	84	Synaptic vesicle protein (SV2)		1180.9	453.4	-1.4	2.60454345
L07073	AAA57231	NP_036227	NM_012095	98	Clathrin-associated adaptor protein homolog (p47A) mRNA		1606.2	1117.2	-1.4	1.4377014
L14851	AAA02856	XP_045648	XM_045648	68	Neurexin III-alpha		1067.3	766.4	-1.4	1.39261482
L19180	S46217	2204414A	U35234	93	Protein tyrosine phosphatase, receptor type, D		5844.8	4314.2	-1.4	1.35478188
L20821	AAA03046	AAG40313	AF318489	89	Syntaxin 4		680.2	266.7	-1.4	2.5504312
L23148	AAA20403	BAA02989	D13890	88	Rattus norvegicus inhibitor of DNA-binding, splice variant Id1.25		1216	855.9	-1.4	1.42072672
L23219	AAA65640	NP_005136	NM_005145	94	G protein gamma subunit (gamma7 subunit)		3491.4	3538.4	-1.4	0.98671716
L24374	AAA99432	NP_002414	NM_002423	70	Matrilysin (MMP-7)		1801.4	1304.2	-1.4	1.38122987
L27075					ATP-citrate lyase		3709.9	2631.3	-1.4	1.40991145
L27340	AAA20999	NP_000184	NM_000193	82	Rat (vhh-1) mRNA		3200.9	2211.3	-1.4	1.44751956
L35271	AAA66191	I38922	U19601	86	AML1		2030.4	1442.3	-1.4	1.40775151
M10094	I54531	I38874	I38874	75	RT1 class Ib gene		2523.9	1869.4	-1.4	1.35011234
M11596	AAA40850	NP_000719	NM_000728	63	Beta-type calcitonin gene-related peptide		2741.1	2005.4	-1.4	1.36685948
M12156	AAA41314	AAH12158	BC012158	89	Rat helix-destabilizing protein		2251.1	1634.1	-1.4	1.37757787

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

M13100					Long interspersed repetitive DNA sequence LINE3		8641.9	6184.1	-1.4	1.39743859
M13100					Long interspersed repetitive DNA sequence LINE3		1791.6	1315.9	-1.4	1.36150163
M13100					Long interspersed repetitive DNA sequence LINE3		1568.5	1095.1	-1.4	1.43228929
M13101					Long interspersed repetitive DNA sequence LINE4		7669.1	5564.4	-1.4	1.37824384
M15562	AAA41609	AAA59783	M60334	64	MHC class II alpha chain RT1.D alpha (u)		5691.7	4324.5	-1.4	1.31615216
M15562	AAA41609	AAA59783	M60334	64	MHC class II alpha chain RT1.D alpha (u)		2837.6	2015.6	-1.4	1.40781901
M15880	P07808	P01303	K01911	93	Neuropeptide Y		2468.6	1777.8	-1.4	1.38857014
M15882	AAA40868	NP_009027	NM_007096	89	Clathryn light chain (LCA1).		18014.4	15928.6	-1.4	1.13094685
M15882	AAA40868	NP_009027	NM_007096	89	Clathryn light chain (LCA1).		10025.6	7295.4	-1.4	1.37423582
M16112	AAA41866	AAD42035	AF078803	95	Brain type II Ca2+/calmodulin-dependent protein kinase		11471.5	6065.8	-1.4	1.89117676
M17526	AAA40826	NP_066268	NM_020988	98	GTP-binding protein		26119.3	18325.1	-1.4	1.42532919
M18416	AAA61927	NP_001955	NM_001964	72	Nerve growth factor-induced protein		1039	471.6	-1.4	2.20313825
M18530	g204785	g425520	S65921	70	Anti-acetylcholine receptor antibody gene, kappa-chain, VJC region		2234.6	1618	-1.4	1.38108776
M23601	AAA41566	NP_000889	NM_000898	83	Rat monoamine oxidase B (Maobf3)		3465.1	2131.2	-1.4	1.62589152
M24542	AAA42051	NP_005994	NM_006003	85	Rat Rieske iron-sulfur protein mRNA, complete cds	AI103911	13029.7	7718.1	-1.4	1.68820046
M25350	AAA41846	AAA03589	L20966	96	cAMP phosphodiesterase (PDE4)		548.2	448.5	-1.4	1.21783724
M27925	AAA42100	NP_003169	NM_003178	81	synapsin 2a		2831.7	1698.5	-1.4	1.66914235
M31032	AAA40969	NP_009175	NM_007244	84n	Rat contiguous repeat polypeptides (CRP) mRNA, complete cds		1177.8	862.3	-1.4	1.36588194
M31174	AAA41121	XP_050014	XM_050014	93	Rat c-erbA-alpha-2-related protein		10557	7739.2	-1.4	1.36409448
M31178	AAA40851	NP_004920	NM_004929	98	Rat calbindin D28		1341.9	973.6	-1.4	1.37828677
M32783	AAA41117	NP_077722	NM_024411	59	Dynorphin		15229.7	10570.3	-1.4	1.44080111
M33648	AAA41336	NP_005509	NM_005518	88	Mitochondrial 3-hydroxy-3-methylglutaryl-CoA synthase		2680.7	1860.5	-1.4	1.44084923
M34043	AAA42062	NP_066932	NM_021109	100	Thymosin beta-4 mRNA		126156.3	89623.7	-1.4	1.40762209
M38135	AAA63484	XP_044593	XM_044593	80	Cathepsin H (RCHII)		3269.1	2367.3	-1.4	1.38094031

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

M57428	AAA42103	AAA36411	M60725	99	Rat S6 kinase mRNA	1719.5	678.6	-1.4	2.53389331
M57728	AAA41632	XP_054752	XM_054752	83	Rat general mitochondrial matrix processing protease (MPP) mRNA, 3' end	738.3	1293.2	-1.4	0.57090937
M58758	AAA41962	NP_005168	NM_005177	91	Rat proton pump polypeptide	5517.4	3892.3	-1.4	1.41751664
M59786	AAA85463	CAA84341	Z34810	85	Rat dihydropryridine-sensitive calcium channel alpha-1 subunit	3584.9	2621.7	-1.4	1.3673952
M61177	AAA63486	AAA36142	M84490	98	Rat extracellular-signal-regulated kinase 1 (ERK1)	38589.2	28547.8	-1.4	1.35173989
M62642	AAA41337	NP_000604	NM_000613	75	Rat (clone pRHx1) hemopexin mRNA	824	576.7	-1.4	1.42881914
M62992	AAA41789	XP_008986	XM_008986	57	Glycoprotein p62	1474.1	1284.3	-1.4	1.14778479
M63485	AAB63955	XP_038204	XM_038204	84	Matrin 3	3243.1	2371.3	-1.4	1.36764644
M64301	AAA41125	AAL17605	AF420474	96	Extracellular signal-related kinase (ERK3)	2741.4	1959.6	-1.4	1.39895897
M69246	AAA41270	NP_004344	NM_004353	85	Collagen-binding protein (gp46)	5770.5	3994.6	-1.4	1.44457518
M76110	AAA42305	NP_001602	NM_001611	83	Tartrate-resistant acid phosphatase type 5	3263.1	2251.2	-1.4	1.4494936
M80804	AAA73144	AAB26524		76	Unknown Protein	7923.4	5815.7	-1.4	1.36241553
M81639		AAC83231	AF070673	90	Stannin mRNA	4341.8	3151.2	-1.4	1.37782432
M81766	AAA42025	AAA60293	M84820	86	Nuclear receptor co-regulator 1 (RCoR-1)	2163.2	1548.7	-1.4	1.3967844
M89945		XP_053253	XM_053253	84	Farnesyl diphosphate synthase	27448.4	19259.5	-1.4	1.42518757
M91595	AAA91899	XP_002636	XM_002636	64	Insulin-like growth factor binding protein-2 gene, exon 1	3442.9	2382.1	-1.4	1.44532136
M95768	AAA40924	NP_004379	NM_004388	82	di-N-acetylchitobiase	964.7	707.7	-1.4	1.36314823
S45812	1903159A	P21397	M68840	91	ESTs, Highly similar to 1903159A monoamine oxidase A [R.norvegicus]	3306.3	2345.7	-1.4	1.40951528
S50461		XP_004753	XM_004753	89	G alpha 12z,=signal-transducing G protein alpha 12 subunit	2362.2	1658.7	-1.4	1.42412733
S54008	Q04589	1EVTC	M37722	97	FGF receptor-1	6398.6	4604.6	-1.4	1.38961039
S55223	AAA13843	NP_003395	NM_003404	98	14-3-3 protein beta subtype	33556.7	22635.6	-1.4	1.48247451
S65555	AAB28225	NP_002052	NM_002061	92	Gamma-glutamylcysteine synthetase light chain	1710.3	1254.2	-1.4	1.36365811
S75019	AAB31867	AAH02515	BC002515	83	Antiquitin=26g turgor protein homolog	2609.6	1805.8	-1.4	1.44512128
S75991		NP_002967	NM_002976	86	Voltage-dependent sodium channel alpha subunit	9546.1	6751.4	-1.4	1.41394377

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

NM_017061	NP_058757	Homology too low for humans				S77494				
					Lysyl oxidase		683.2	1425.4	-1.4	0.47930406
S79263	AAB35068	XP_009960	XM_009960	49	rIL-3R beta =interleukin-3 receptor beta-subunit		7642.6	5320.2	-1.4	1.43652494
U00926	AAC28872	AAH02389	BC002389	70	Delta subunit of F1F0 ATPase		22572.8	12558.7	-1.4	1.79738349
U02096	AAA60455	NP_001437	NM_001446	88	Fatty acid binding protein mRNA		4252	3029.7	-1.4	1.40343928
U05989	AAA16492	NP_002574	NM_002583	69	Rattus norvegicus clone par-4 induced by effectors of apoptosis		986	534	-1.4	1.84644195
U06230	I59618	P07225	J02917	75	Protein S		559.2	615.6	-1.4	0.90838207
U08214	AAA81950	XP_050405	XM_050405	91	DNA binding protein (URE-B1)		5544.7	4051.2	-1.4	1.3686562
U13396	AAA79911	XP_038595	XM_038595	48	Protein-tyrosine kinase (JAK2)		817.7	581.2	-1.4	1.40691672
U14746	AAA86874	NP_000542	NM_000551	87	VHL protein		2897.9	2058.5	-1.4	1.40777265
U17834	AAA58797	NP_001702	NM_001711	96	Biglycan		6516.1	2372.6	-1.4	2.74639636
U17837	AAA74468	AAC50820	U17838	67	Rattus sp. zinc finger protein RIZ mRNA		6244.6	5843.4	-1.4	1.06865866
U17919	AAA80105	NP_001614	NM_001623	89	Allograft inflammatory factor-1		961.5	707.3	-1.4	1.35939488
U24150	AAC52289	CAA53287	X75621	84	Tuberous sclerosis 2 homolog		2575.3	1892.4	-1.4	1.36086451
U24489	g1336153	g180964	M26856	70	Tenascin X		9663.9	5845.9	-1.4	1.65310731
U27562	AAA68708	CAA60386	X86693	60	SC1 protein		9422.2	6935.2	-1.4	1.35860538
U30381	Q62806	Q9UQR1	AF039019	97	Zinc finger protein 148		1215.3	869.3	-1.4	1.3980214
U30788					Rattus norvegicus Tclone4 mRNA		2286	822.4	-1.4	2.77966926
U33540				No Human	Cytochrome P450 (CYP2B14P) pseudogene		2614.4	2554.3	-1.4	1.02352895
U35099	BAA11086	AAC50229	U35100	100	Rattus norvegicus complexin II mRNA, complete cds		848.5	828.4	-1.4	1.02426364
U41164	AAB61447	XP_044307	XM_044307	68	Rattus norvegicus Cys2/His2 zinc finger protein (rKr1)		8503.5	6252.8	-1.4	1.35995074
U42627	AAB06202	XP_017018	XM_017018	83	Dual-specificity protein tyrosine phosphatase		1323.9	650.7	-1.4	2.03457815
U47031	AAA99777	CAA68948	Y07684	84	P2x4 ATP receptor		1359.1	574.5	-1.4	2.36570931
U48288	AAB06559	NP_057332	NM_016248	62	Rattus norvegicus A-kinase anchoring protein AKAP 220		3173.3	2285.8	-1.4	1.38826669
U50842	AAB48949	BAA07655	D42055	78	Ubiquitin ligase (Nedd4) protein		14754.3	10457.9	-1.4	1.41082818
U57391	AAC52601	AAF73912	AF227967	65	FceRI gamma-chain interacting protein SH2-B		7744	5719.8	-1.4	1.35389349
U61729	AAB09057	NP_006804	NM_006813	62	Proline rich protein		753.2	540	-1.4	1.39481481
U70825	P97608	g5419885	AL096750	93	5-oxo-L-prolinase		772.6	560.3	-1.4	1.37890416

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

U75400	AAB38315	NP_004757	NM_004766	50	Coatomer beta subunit mRNA		1787.6	1245	-1.4	1.43582329
Z78279	CAB01633	AAB27856	S64596	85	Alpha 1 type I collagen	U75405	54964.4	39299.2	-1.4	1.39861371
U75920	AAB81885	NP_036457	NM_012325	95	APC binding protein EB1 mRNA		1320.7	976.3	-1.4	1.35276042
U82623	AAB91537	NP_006779	NM_006788	71	Cytocentrin		2172.7	1539	-1.4	1.41176088
U84727	AAB41797	CAA46905	X66114	96	2-oxoglutarate carrier		7094.8	4994.9	-1.4	1.42040882
U91561	AAC23707	NP_060599	NM_018129	89	Pyridoxine 5'-phosphate oxidase		1512.5	1086.7	-1.4	1.39182847
U92802	AAC53208	AAH11634	BC011634	83	Orphan G-protein coupled receptor (GPR41)		633.5	235.6	-1.4	2.68887946
U94340	AAC53544	AAA60137	M18112	82	Poly(ADP-ribose) polymerase		2588.8	1792.5	-1.4	1.44423989
X05300	A27274	A26168	Y00281	94	Ribophorin I		4082.1	3868.5	-1.4	1.0552152
X05472					Rat 2.4 kb repeat DNA right terminal region		1069.5	1084.8	-1.4	1.00441397
X06832	CAA29988	AAA52017	J03483	53	Prechromogranin A		3133.2	2319.5	-1.4	1.35080836
X07365	CAB43593	CAB37833	Y00483	86	Glutathione peroxidase		10685.9	7853.9	-1.4	1.36058519
X12355	CAA30916	BAA11928	D83485	91	Phosphoinositide-specific phospholipase C form-I		8585.2	6297.7	-1.4	1.36322785
X12554	CAA31068	AAA52062	M83308	80	Heart cytochrome c oxidase subunit VIa		2756.5	1917.9	-1.4	1.43724907
X13411	CAA31777	XP_045572	XM_045572	98	Elk protein		3227.1	2371	-1.4	1.36107128
X13527	CAA31882	AAA73576	U29344	77	Acyl carrier protein domain of fatty acid synthetase		4495.4	3234	-1.4	1.39004329
X13983	CAA32164	XP_006925	XM_006925	67	Rat alpha-2-macroglobulin		8250.5	5950.9	-1.4	1.38642894
X14181	CAA32385	NP_000971	NM_000980	99	Ribosomal protein L18a (AA 1-175)		19578.3	13697	-1.4	1.429386
X17012	P01346	IGHU2	X00910	90	Insulin-like growth factor II (somatomedin A)		2696.3	1897.5	-1.4	1.42097497
X51707	CAA36003	NP_001013	NM_001022	99	Ribosomal protein S19		21837.1	15405.6	-1.4	1.41747806
X52840	CAA37024	XP_041677	XM_041677	93	Smooth muscle myosin RLC-B		888.9	631.7	-1.4	1.4071553
NM_022399	NP_071794	XP_032021	XM_032021	87	Calreticulin	X53363	4606	3244.1	-1.4	1.41980827
X56596	CAA39934	CAA60790	X87344	65	MHC class II antigen RT1.B-1 beta-chain		2144.1	302.3	-1.4	7.09262322
X60468	CAA42998	NP_001155	NM_001164	89	Integrase-like protein, APP interacting protein		4979.8	5198.2	-1.4	0.95798546
X66022		XP_009172	XM_009172	93	Neuro-D4 protein		534.4	423.9	-1.4	1.26067469
X67877	CAA48076	XP_037004	XM_037004	67	cytosolic resiniferatoxin binding protein RBP-26		1266.4	763.1	-1.4	1.65954659
X70223	CAA49756	NP_061133	NM_018663	72	22kDa integral peroxisomal membrane		1073.4	768.1	-1.4	1.39747429
X74226	CAA52297	BAB55164	AK027510	75	LL5 mRNA		4207.5	3063.3	-1.4	1.37351875

Table 5. Polynucleotide Seqences Which are Downregulated Following Inflammation

X74800	CAA52807	O00159	X98507	91	MYR2 mRNA for myosin I heavy chain		1483.7	1051.6	-1.4	1.41089768
X76489	CAA54027	NP_001760	NM_001769	79	CD9 mRNA for cell surface glycoprotein		27449.1	19594.3	-1.4	1.40087168
X89968	CAA62005	XP_038976	XM_038976	90	Alpha-soluble NSF attachment protein		14212	10308.6	-1.4	1.37865472
X90823	CAA62338	CAA62341	X90826	93	USF2a & USF2b		968.6	847.6	-1.4	1.14039841
X93591	CAA63789	XP_034901	XM_034901	90	Mismatch repair protein, MSH2		1693	954.9	-1.4	1.77296052
Y13336	CAA73780	NP_001335	NM_001344	88	DAD-1 gene		15870.7	11180.5	-1.4	1.41949823
Z18877	CAA79317	P00973	D00068	65	R.norvegicus mRNA for 2'5' oligoadenylate synthetase		5135	2231.4	-1.4	2.30124585

Table 8. Differentially Expressed Sequences Validated by Northern

#	Descriptions	Accession number	Axotomy: Naive Intensity	Axotomy: Axotomy Intensity	Axotomy: Fold change	Northern: Regulation	Spared Nerve Injury: NI Intensity	Spared Nerve Injury: SNI Intensity	Spared Nerve Injury: Fold change
1	GTP cyclohydrolase I	M58364	#	(+)	↑↑↑	↑↑↑	#	+	↑↑
2	Guanine nucleotide-releasing protein (MSS4)	L10336	#	(++)	-	NC	(+)	+	-
3	Enkephalinase (neutral endopeptidase)	M15944	#	(+)	↑	↑	+	(+)	↓↓
4	Cholecystokinin receptor (CCK-B)	M99418	#	(+)	↑↑	↑↑↑	#	(+)	↑↑
5	Endothelin-1	M64711	#	(+)	↑↑	↑↑	#	(+)	-
6	Cannabinoid CB1 receptor	X55812	(+)	(+)	↑	↓↓	(+)	#	↓
7	53 kD polypeptide	X02601	(+)	+	↑	↑↑↑	#	+	-
8	ET-B endothelin receptor	X57764	(+)	+	-	NC	+	(+)	-
9	Metallothionein-1 (EST211851)	AI102562	+	++	↑↑	↑↑	++	+	↓
10	Small proline-rich protein (EST195714)	AA891911	(+)	++	↑↑	↑↑↑	(+)	+	↑
11	Immediate-early serum-responsive JE (IES-JE)	X17053	+	++	↑↑	↑↑	++	++	-
12	5HT-3	U59672	+	#	↓	↓↓	+	+	↓↓
13	Peripheral-type benzodiazepine receptor	J05122	++	++	↑	↑	(+)	++	↑↑
14	α-2-macroglobulin	M23566	(++)	+++	↑↑	↑↑	++	++	↓
15	Pituitary adenylate cyclase activating peptide	X80290	++	++	↑↑	↑↑	++	++	↑↑
16	GFRα1 (RET ligand 1)	U97142	++	++	↑↑	↑	+	++	↑↑
17	HNF-3/fork-head homolog-2 (HFH-2)	L13202	(++)	++	-	NC	++	++	↓
18	Calcium channel α-2 subunit (CCHL2A)	M86621	++	+++	↑↑↑	↑↑	++	++++	↑↑↑
19	CLP36	U23769	++	++	↑↑	↑↑	++	++	↑↑
20	VGF	M74223	++	+++	↑↑	↑↑	(+)	+++	↑↑↑
21	gadd45	L32591	++	+++	↑↑	↑↑	+	+++	↑↑↑
22	Guanine nucleotide-binding protein G-I, α subunit	M12672	+++	+++	-	NC	+++	+++	-
23	Lysozyme (EST196578)	AA892775	+++	++++	↑↑	↑	+++	++++	↑
24	Phopholemman chloride channel (EST189142)	AA799645	+++	++++	↑↑	↑	++	+++	-
25	SNAP-25A	AB003991	++++	+++	↑↑	↓	++++	+++	↓

KEY

- = < 1.4 fold	# = below detection	( ) = present only on 1 chip
↑ = 1.4 < < 2 fold	+ = 100 - 1000	NC = no change
↑↑ = 2 < < 5 fold	++ = 1000 - 5000	↑ = slight regulation
↑↑↑ = > 5 fold	+++ = 5000 - 10.000	↑↑ = moderate/high regulation
	++++ = >10.000	↑↑↑ = induced

Table 9. Differentially Expressed Sequences Validated by TaqMan

#	Descriptions	Accession Number	Axotomy			Taqman data		Spared Nerve Injury		
			Naive Intensity	Axotomy Intensity	Fold change	1 day Axotomy regulation/ fold change	5 day Axotomy regulation/ fold change	Naive Intensity	SNI Intensity	Fold change
1	c-jun	X17163	#	#		↑ x5.2	↑ x3.7	#	++	▲▲▲
2	mGluR5	D10891	#	#		NC	NC	#	#	
3	NK1 receptor	M64236	#	#		NC	NC	(+)	#	▼
4	Cyclooxygenase 2	S67722	#	#		NC	NC	#	#	
5	c-fos	X06769	#	#		↑ x3.2	NC	#	(+)	▲
6	mGluR1	M61099	#	(+)	-	NC	NC	#	#	
7	μ-opioid receptor (MOR)	S77863	#	#		NC	↓ x2.3	#	#	
8	Galanin	J03624	#	++++	▲▲▲	↑ x10	↑ x62.	#	+++	▲▲▲
9	Neuronal nitric oxide synthase	U67309	#	#		NC	↑ x4	#	#	
10	Cannabinoid CB1 receptor	X55812	(+)	(+)	▲	NC	↓ x1.8	(+)	#	-
11	Brain-derived neurotrophic factor	D10938	+	(+)	-	↑ x2.7	NC	+	+	▲
12	Cyclooxygenase 1	U03388	(+)	#	-	NC	NC	#	(+)	-
13	Vanilloid receptor subtype 1	AF029310	++	(++)	-	↓ x1.6	↓ x2.9	++	+	▼
14	Leucine zipper protein (ATF3)	M63282	++	+++	▲▲▲	↑ x31	↑ x20	+	++	▲▲▲
15	Calcitonin gene-related peptide (beta)	M11596	++	(+)	▼▼▼	NC	↓ x2	++	++	▼▼
16	Voltage-gated Na channel α subunit Nav 1.9	AF059030	+++	++	▼	NC	↓ x2.4	+++	++	▼▼
17	Dynorphin	M32783	+++	+++	-	NC	NC	++	++	▼
18	Neuron-specific enolase	X07729	+++	+++	-	NC	NC	+++	+++	-
19	GAP-43	L21192	+++	++++	▲▲	↑ x3.3	↑ x2	+++	++++	▲
20	TrkA	M85214	+++	+++	-	NC	↓ x1.4	+++	++	▼▼
21	Heat shock protein 27	M86389	++++	++++	▲▲	↑ x1.8	↑ x1.8	+++	++++	▲▲

KEY

NC = no change
\- = < 1.4 fold
▲ = 1.4 < < 2 fold
▲▲ = 2 < < 5 fold
▲▲▲ = > 5 fold

( ) = present only on 1 chip
\# = below detection
\+ = 100 - 1000
++ = 1000 - 5000
+++ = 5000 - 10.000
++++ = >10.000

Vectors and Host Cells

In addition to providing genes which are differentially expressed in animals which have been subjected to pain, the present invention further provides vectors and plasmids useful for directing the expression of differentially expressed genes, or therapeutic nucleic acid constructs, and further provides host cells which express the vectors and plasmids provided herein. Nucleic acid sequences useful for the expression from a vector or plasmid as described below include, but are not limited to any nucleic acid or gene sequence identified as being differentially regulated by the methods described above, and further include therapeutic nucleic acid molecules, such as antisense molecules. The host cell may be any prokaryotic or eukaryotic cell. Ligating the polynucleotide sequence into a gene construct, such as an expression vector, and transforming or transfecting into hosts, either eukaryotic (yeast, avian, insect or mammalian) or prokaryotic (bacterial cells), are standard procedures well known in the art.

Vectors

There is a wide array of vectors known and available in the art that are useful for the expression of differentially expressed nucleic acid molecules according to the invention. The selection of a particular vector clearly depends upon the intended use the polypeptide encode the differentially expressed nucleic acid. For example, the selected vector must be capable of driving expression of the polypeptide in the desired cell type, whether that cell type be prokaryotic or eukaryotic. Many vectors comprise sequences allowing both prokaryotic vector replication and eukaryotic expression of operably linked gene sequences.

Vectors useful according to the invention may be autonomously replicating, that is, the vector, for example, a plasmid, exists extrachromosomally and its replication is not necessarily directly linked to the replication of the host cell's genome. Alternatively, the replication of the vector may be linked to the replication of the host's chromosomal DNA, for example, the vector may be integrated into the chromosome of the host cell as achieved by retroviral vectors.

Vectors useful according to the invention preferably comprise sequences operably linked to the differentially expressed sequences that permit the transcription and translation of the sequence. Sequences that permit the transcription of the linked differentially expressed sequence include a promoter and optionally also include an enhancer element or elements permitting the strong expression of the linked sequences. The term "transcriptional regulatory sequences" refers to the combination of a promoter and any additional sequences conferring desired

expression characteristics (e.g., high level expression, inducible expression, tissue- or cell-type-specific expression) on an operably linked nucleic acid sequence.

The selected promoter may be any DNA sequence that exhibits transcriptional activity in the selected host cell, and may be derived from a gene normally expressed in the host cell or from a gene normally expressed in other cells or organisms. Examples of promoters include, but are not limited to the following: A) prokaryotic promoters - *E. coli* lac, tac, or trp promoters, lambda phage P_R or P_L promoters, bacteriophage T7, T3, Sp6 promoters, *B. subtilis* alkaline protease promoter, and the *B. stearothermophilus* maltogenic amylase promoter, etc.; B) eukaryotic promoters - yeast promoters, such as GAL1, GAL4 and other glycolytic gene promoters (see for example, Hitzeman et al., 1980, J. Biol. Chem. 255: 12073-12080; Alber & Kawasaki, 1982, J. Mol. Appl. Gen. 1: 419-434), LEU2 promoter (Martinez-Garcia et al., 1989, Mol Gen Genet. 217: 464-470), alcohol dehydrogenase gene promoters (Young et al., 1982, in Genetic Engineering of Microorganisms for Chemicals, Hollaender et al., eds., Plenum Press, NY), or the TPI1 promoter (U.S. Pat. No. 4,599,311); insect promoters, such as the polyhedrin promoter (U.S. Pat. No. 4,745,051; Vasuvedan et al., 1992, FEBS Lett. 311: 7-11), the P10 promoter (Vlak et al., 1988, J. Gen. Virol. 69: 765-776), the *Autographa californica* polyhedrosis virus basic protein promoter (EP 397485), the baculovirus immediate-early gen promoter gene 1 promoter (U.S. Pat. Nos. 5,155,037 and 5,162,222), the baculovirus 39K delayed-early gene promoter (also U.S. Pat. Nos. 5,155,037 and 5,162,222) and the OpMNPV immediate early promoter 2; mammalian promoters - the SV40 promoter (Subramani et al., 1981, Mol. Cell. Biol. 1: 854-864), metallothionein promoter (MT-1; Palmiter et al., 1983, Science 222: 809-814), adenovirus 2 major late promoter (Yu et al.,1984, Nucl. Acids Res. 12: 9309-21), cytomegalovirus (CMV) or other viral promoter (Tong et al., 1998, Anticancer Res. 18: 719-725), or even the endogenous promoter of a gene of interest in a particular cell type.

A selected promoter may also be linked to sequences rendering it inducible or tissue-specific. For example, the addition of a tissue-specific enhancer element upstream of a selected promoter may render the promoter more active in a given tissue or cell type. Alternatively, or in addition, inducible expression may be achieved by linking the promoter to any of a number of sequence elements permitting induction by, for example, thermal changes (temperature sensitive), chemical treatment (for example, metal ion- or IPTG-inducible), or the addition of an antibiotic inducing agent (for example, tetracycline).

Regulatable expression is achieved using, for example, expression systems that are drug inducible (e.g., tetracycline, rapamycin or hormone-inducible). Drug-regulatable promoters that are particularly well suited for use in mammalian cells include the tetracycline regulatable promoters, and glucocorticoid steroid-, sex hormone steroid-, ecdysone-, lipopolysaccharide (LPS)- and isopropylthiogalactoside (IPTG)-regulatable promoters. A regulatable expression system for use in mammalian cells should ideally, but not necessarily, involve a transcriptional regulator that binds (or fails to bind) nonmammalian DNA motifs in response to a regulatory agent, and a regulatory sequence that is responsive only to this transcriptional regulator.

Tissue-specific promoters may also be used to advantage in differentially expressed sequence-encoding constructs of the invention. A wide variety of tissue-specific promoters is known. As used herein, the term "tissue-specific" means that a given promoter is transcriptionally active (i.e., directs the expression of linked sequences sufficient to permit detection of the polypeptide product of the promoter) in less than all cells or tissues of an organism. A tissue specific promoter is preferably active in only one cell type, but may, for example, be active in a particular class or lineage of cell types (e.g., hematopoietic cells). A tissue specific promoter useful according to the invention comprises those sequences necessary and sufficient for the expression of an operably linked nucleic acid sequence in a manner or pattern that is essentially the same as the manner or pattern of expression of the gene linked to that promoter in nature. The following is a non-exclusive list of tissue specific promoters and literature references containing the necessary sequences to achieve expression characteristic of those promoters in their respective tissues; the entire content of each of these literature references is incorporated herein by reference. Examples of tissue specific promoters useful in the present invention are as follows:

Bowman et al., 1995 Proc. Natl. Acad. Sci. USA 92,12115-12119 describe a brain-specific transferrin promoter; the synapsin I promoter is neuron specific (Schoch et al., 1996 J. Biol. Chem. 271, 3317-3323); the nestin promoter is post-mitotic neuron specific (Uetsuki et al., 1996 J. Biol. Chem. 271, 918-924); the neurofilament light promoter is neuron specific (Charron et al., 1995 J. Biol. Chem. 270, 30604-30610); the acetylcholine receptor promoter is neuron specific (Wood et al., 1995 J. Biol. Chem. 270, 30933-30940); and the potassium channel promoter is high-frequency firing neuron specific (Gan et al., 1996 J. Biol. Chem 271, 5859-5865). Any tissue specific transcriptional regulatory sequence known in the art may be used to

advantage with a vector encoding a differentially expressed nucleic acid sequence obtained from an animal subjected to pain.

In addition to promoter/enhancer elements, vectors useful according to the invention may further comprise a suitable terminator. Such terminators include, for example, the human growth hormone terminator (Palmiter et al., 1983, supra), or, for yeast or fungal hosts, the TPI1 (Alber & Kawasaki, 1982, supra) or ADH3 terminator (McKnight et al., 1985, EMBO J. 4: 2093-2099).

Vectors useful according to the invention may also comprise polyadenylation sequences (e.g., the SV40 or Ad5E1b poly(A) sequence), and translational enhancer sequences (e.g., those from Adenovirus VA RNAs). Further, a vector useful according to the invention may encode a signal sequence directing the recombinant polypeptide to a particular cellular compartment or, alternatively, may encode a signal directing secretion of the recombinant polypeptide.

a. Plasmid vectors.

Any plasmid vector that allows expression of a differentially expressed coding sequence of the invention in a selected host cell type is acceptable for use according to the invention. A plasmid vector useful in the invention may have any or all of the above-noted characteristics of vectors useful according to the invention. Plasmid vectors useful according to the invention include, but are not limited to the following examples: Bacterial - pQE70, pQE60, pQE-9 (Qiagen) pBs, phagescript, psiX174, pBluescript SK, pBsKS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, and pRIT5 (Pharmacia); Eukaryotic - pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, and pSVL (Pharmacia). However, any other plasmid or vector may be used as long as it is replicable and viable in the host.

b. Bacteriophage vectors.

There are a number of well known bacteriophage-derived vectors useful according to the invention. Foremost among these are the lambda-based vectors, such as Lambda Zap II or Lambda-Zap Express vectors (Stratagene) that allow inducible expression of the polypeptide encoded by the insert. Others include filamentous bacteriophage such as the M13-based family of vectors.

c. Viral vectors.

A number of different viral vectors are useful according to the invention, and any viral vector that permits the introduction and expression of one or more of the differentially expressed polynucleotides of the invention in cells is acceptable for use in the methods of the invention. Viral vectors that can be used to deliver foreign nucleic acid into cells include but are not limited to retroviral vectors, adenoviral vectors, adeno-associated viral vectors, herpesviral vectors, and Semliki forest viral (alphaviral) vectors. Defective retroviruses are well characterized for use in gene transfer (for a review see Miller, A.D. (1990) *Blood* 76:271). Protocols for producing recombinant retroviruses and for infecting cells *in vitro* or *in vivo* with such viruses can be found in Current Protocols in Molecular Biology, Ausubel, F.M. et al. (eds.) Greene Publishing Associates, (1989), Sections 9.10-9.14, and other standard laboratory manuals.

In addition to retroviral vectors, Adenovirus can be manipulated such that it encodes and expresses a gene product of interest but is inactivated in terms of its ability to replicate in a normal lytic viral life cycle (see for example Berkner et al., 1988, BioTechniques 6:616; Rosenfeld et al., 1991, Science 252:431-434; and Rosenfeld et al., 1992, Cell 68:143-155). Suitable adenoviral vectors derived from the adenovirus strain Ad type 5 dl324 or other strains of adenovirus (e.g., Ad2, Ad3, Ad7 etc.) are well known to those skilled in the art. Adeno-associated virus (AAV) is a naturally occurring defective virus that requires another virus, such as an adenovirus or a herpes virus, as a helper virus for efficient replication and a productive life cycle. (For a review see Muzyczka et al., 1992, Curr. Topics in Micro. and Immunol. 158:97-129). An AAV vector such as that described in Traschin et al. (1985, Mol. Cell. Biol. 5:3251-3260) can be used to introduce nucleic acid into cells. A variety of nucleic acids have been introduced into different cell types using AAV vectors (see, for example, Hermonat et al., 1984, Proc. Natl. Acad. Sci. USA 81: 6466-6470; and Traschin et al., 1985, Mol. Cell. Biol. 4: 2072-2081).

Host cells

Any cell into which a recombinant vector carrying a gene encoding a nucleic acid sequence differentially expressed in an animal subjected to pain may be introduced and wherein the vector is permitted to drive the expression of the peptide encoded by the differentially expressed sequence is useful according to the invention. Any cell in which a differentially expressed molecule of the invention may be expressed and preferably detected is a suitable host, wherein the host cell is preferably a mammalian cell and more preferably a human cell. Vectors suitable for the introduction of differentially expressed nucleic acid sequences to host cells from

a variety of different organisms, both prokaryotic and eukaryotic, are described herein above or known to those skilled in the art.

Host cells may be prokaryotic, such as any of a number of bacterial strains, or may be eukaryotic, such as yeast or other fungal cells, insect or amphibian cells, or mammalian cells including, for example, rodent, simian or human cells. Cells may be primary cultured cells, for example, primary human fibroblasts or keratinocytes, or may be an established cell line, such as NIH3T3, 293T or CHO cells. Further, mammalian cells useful in the present invention may be phenotypically normal or oncogenically transformed. It is assumed that one skilled in the art can readily establish and maintain a chosen host cell type in culture.

Introduction of vectors to host cells.

Vectors useful in the present invention may be introduced to selected host cells by any of a number of suitable methods known to those skilled in the art. For example, vector constructs may be introduced to appropriate bacterial cells by infection, in the case of E. coli bacteriophage vector particles such as lambda or M13, or by any of a number of transformation methods for plasmid vectors or for bacteriophage DNA. For example, standard calcium-chloride-mediated bacterial transformation is still commonly used to introduce naked DNA to bacteria (Sambro et al., 1989, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY), but electroporation may also be used (Ausubel et al., 1988, Current Protocols in Molecular Biology, (John Wiley & Sons, Inc., NY, NY)).

For the introduction of vector constructs to yeast or other fungal cells, chemical transformation methods are generally used (e.g. as described by Rose et al., 1990, Methods in Yeast Genetics, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY). For transformation of S. cerevisiae, for example, the cells are treated with lithium acetate to achieve transformation efficiencies of approximately 10^4 colony-forming units (transformed cells)/μg of DNA. Transformed cells are then isolated on selective media appropriate to the selectable marker used. Alternatively, or in addition, plates or filters lifted from plates may be scanned for GFP fluorescence to identify transformed clones.

For the introduction of vectors comprising differentially expressed sequences to mammalian cells, the method used will depend upon the form of the vector. Plasmid vectors may be introduced by any of a number of transfection methods, including, for example, lipid-mediated transfection ("lipofection"), DEAE-dextran-mediated transfection, electroporation or

calcium phosphate precipitation. These methods are detailed, for example, in Current Protocols in Molecular Biology (Ausubel et al., 1988, John Wiley & Sons, Inc., NY, NY).

Lipofection reagents and methods suitable for transient transfection of a wide variety of transformed and non-transformed or primary cells are widely available, making lipofection an attractive method of introducing constructs to eukaryotic, and particularly mammalian cells in culture. For example, LipofectAMINE™ (Life Technologies) or LipoTaxi™(Stratagene) kits are available. Other companies offering reagents and methods for lipofection include Bio-Rad Laboratories, CLONTECH, Glen Research, InVitrogen, JBL Scientific, MBI Fermentas, PanVera, Promega, Quantum Biotechnologies, Sigma-Aldrich, and Wako Chemicals USA.

Following transfection with a vector of the invention, eukaryotic (e.g., human) cells successfully incorporating the construct (intra- or extrachromosomally) may be selected, as noted above, by either treatment of the transfected population with a selection agent, such as an antibiotic whose resistance gene is encoded by the vector, or by direct screening using, for example, FACS of the cell population or fluorescence scanning of adherent cultures. Frequently, both types of screening may be used, wherein a negative selection is used to enrich for cells taking up the construct and FACS or fluorescence scanning is used to further enrich for cells expressing differentially expressed polynucleotides or to identify specific clones of cells, respectively. For example, a negative selection with the neomycin analog G418 (Life Technologies, Inc.) may be used to identify cells that have received the vector, and fluorescence scanning may be used to identify those cells or clones of cells that express the vector construct to the greatest extent.

Polynucleotide arrays comprising differentially expressed nucleic acid sequences

In one embodiment, the present invention provides a pain-specific polynucleotide array comprising nucleic acid sequences that are identified as being differentially expressed in an animal subjected to pain relative to a naïve animal stably associated at discrete predefined regions on a surface. In a preferred embodiment, a pain-specific microarray useful in the present invention comprises one or more polynucleotides shown in Tables 1, 2, 3, 4, or 5. At least one of the polynucleotides comprising a pain-specific array useful in the present invention must be selected from Table 2, 3, 4, or 5. A pain-specific microarray according to the invention preferably comprises between 10 and 20,000 nucleic acid members, and more preferably comprises at least 5000 nucleic acid members. The nucleic acid members are known or novel

polynucleotide sequences which have been determined to be differentially expressed as described herein, or any combination thereof. A pain-specific microarray according to the invention may be used, for example, to test therapeutic compounds which may modulate the expression of the sequences comprising the array in an animal subjected to pain. For example, an animal subjected to pain may be treated with a potentially therapeutic compound as described below. Total RNA may then be extracted from, for example, primary sensory neurons, prepared according to the methods described above, and hybridized to the pain-specific microarray. The level of hybridization of samples to the pain-specific microarray may be compared to the level of hybridization of a nucleic acid sample obtained from an animal subjected to pain, but not administered the therapeutic compound. The pain-specific microarray may also be used, for example, to test the ability of an antisense nucleic acid to hybridize to the differentially expressed nucleic acid molecules comprising the pain-specific microarray. The antisense molecules may then be used to inhibit the expression of, for example, nucleic acid sequences which have been identified, using the above methods, as being upregulated (i.e., by at least 1.4 fold) in an animal subjected to pain.

The invention also provides for a pain-specific microarray comprising nucleic acids sequences which have been identified and verified as being differentially expressed in an ani subjected to pain, wherein the sequences stably associated with the array are obtained from at least two different species of animal. In a preferred embodiment, a pain-specific microarray useful in the present invention comprises at least one polynucleotide shown in Table 2, 3, 4, or 5, and may optionally further comprise one or more of the polynucleotides shown in Table 1. Such arrays may also be used for prognostic methods to monitor an animal's response to therapy. In one embodiment, the above pain-specific microarrays are used to identify a therapeutic agent that changes (e.g., increases or decreases) the level of expression of at least one polynucleotide sequence that is differentially expressed (i.e., by at least 1.4 fold, or at least 1.2 fold in combination with a p-value of less than 0.05 in triplicate analysis) in sensory neurons in an animal subjected to pain.

The nucleic acid samples that are hybridized to and analyzed with a pain-specific microarray of the invention are preferably derived from sensory neurons of an animal subjected to pain (or from a naïve control animal). More preferably, the nucleic acid samples are obtained from primary sensory neurons of the dorsal root ganglion. A limitation for this procedure lies in

the amount of RNA available for use as a probe nucleic acid sample. Preferably, at least 1 microgram of total RNA is obtained for use according to this invention.

Construction of a pain-specific microarray

An aspect of the present invention incorporates the previously identified differentially regulated nucleic acid sequences into a pain-specific polynucleotide microarray. In the present methods, an array of nucleic acid members stably associated with the surface of a substantially planar solid support is contacted with a sample comprising probe polynucleotides obtained from an animal subjected to pain, or from a naïve animal under hybridization conditions sufficient to produce a hybridization pattern of complementary nucleic acid members/probe complexes.

The nucleic acid members may be produced using established techniques such as polymerase chain reaction (PCR) and reverse transcription (RT). For example, once a nucleic acid sequence has been identified as being differentially expressed in an animal subjected to pain, the sequence may be amplified from the originally obtained RNA sample by RT-PCR, wherein the amplified product may be used to construct a pain-specific microarray. These methods are similar to those currently known in the art (see e.g. PCR Strategies, Michael A. Innis (Editor), et al. (1995) and PCR: Introduction to Biotechniques Series, C. R. Newton, A. Graham (1997)). Amplified polynucleotides are purified by methods well known in the art (e.g., column purification or alcohol precipitation). A polynucleotide is considered pure when it has been isolated so as to be substantially free of primers and incomplete products produced during the synthesis of the desired polynucleotide. Preferably, a purified polynucleotide will also be substantially free of contaminants which may hinder or otherwise mask the binding activity of the molecule.

A pain-specific microarray according to the invention comprises a plurality of unique polynucleotides attached to one surface of a solid support at a density exceeding 20 different polynucleotides/cm^2, wherein each of the polynucleotides is attached to the surface of the solid support in a non-identical preselected region. Each associated sample on the array comprises a polynucleotide composition, of known identity, usually of known sequence, as described in greater detail below. Any conceivable substrate may be employed in the invention. In one embodiment, the polynucleotide attached to the surface of the solid support is DNA. In a preferred embodiment, the polynucleotide attached to the surface of the solid support is cDNA or RNA. In another preferred embodiment, the polynucleotide attached to the surface of the solid

support is cDNA synthesized by polymerase chain reaction (PCR). Preferably, a nucleic acid member comprising an array, according to the invention, is at least 25 nucleotides in length. In one embodiment, a nucleic acid member comprising an array is at least 150 nucleotides in length. Preferably, a nucleic acid member comprising an array is less than 1000 nucleotides in length. More preferably, a nucleic acid member comprising an array is less than 500 nucleotides in length. In one embodiment, an array comprises at least 10 different polynucleotides attached to one surface of the solid support. In another embodiment, the array comprises at least 100 different polynucleotides attached to one surface of the solid support. In yet another embodiment, the array comprises at least 10000 different polynucleotides attached to one surface of the solid support.

In the arrays of the invention, the polynucleotide compositions are stably associated with the surface of a solid support, wherein the support may be a flexible or rigid solid support. By "stably associated" is meant that each nucleic acid member maintains a unique position relative to the solid support under hybridization and washing conditions. As such, the samples are non-covalently or covalently stably associated with the support surface. Examples of non-covalent association include non-specific adsorption, binding based on electrostatic interactions (e.g., ion pair interactions), hydrophobic interactions, hydrogen bonding interactions, specific binding through a specific binding pair member covalently attached to the support surface, and the like. Examples of covalent binding include covalent bonds formed between the polynucleotides and a functional group present on the surface of the rigid support (e.g., --OH), where the functional group may be naturally occurring or present as a member of an introduced linking group, as described in greater detail below

The amount of differentially expressed polynucleotide present in each composition will be sufficient to provide for adequate hybridization and detection of probe polynucleotide sequences during the assay in which the array is employed. Generally, the amount of each nucleic acid member stably associated with the solid support of the array is at least about 0.1 ng, preferably at least about 0.5 ng and more preferably at least about 1 ng, where the amount may be as high as 1000 ng or higher, but will usually not exceed about 20 ng. Where the nucleic acid member is "spotted" onto the solid support in a spot comprising an overall circular dimension, the diameter of the "spot" will generally range from about 10 to 5,000 μm, usually from about 20 to 2,000 μm and more usually from about 50 to 1000 μm.

Control nucleic acid members may be present on the array including nucleic acid members comprising oligonucleotides or polynucleotides corresponding to genomic DNA, housekeeping genes, vector sequence, plant nucleic acid sequence, negative and positive control genes, and the like. Control nucleic acid members are calibrating or control genes whose function is not to tell whether a particular "key" gene of interest is expressed, but rather to provide other useful information, such as background or basal level of expression.

Other control polynucleotides are spotted on the array and used as probe expression control polynucleotides and mismatch control nucleotides to monitor non-specific binding or cross-hybridization to a polynucleotide in the sample other than the target to which the probe is directed. Mismatch probes thus indicate whether a hybridization is specific or not. For example, if the target is present, the perfectly matched probes should be consistently brighter than the mismatched probes.

Solid substrate

An array according to the invention comprises either a flexible or rigid substrate. A flexible substrate is capable of being bent, folded or similarly manipulated without breakage. Examples of solid materials which are flexible solid supports with respect to the present invention include membranes, e.g., nylon, flexible plastic films, and the like. By "rigid" is meant that the support is solid and does not readily bend, i.e., the support is not flexible. As such, the rigid substrates of the subject arrays are sufficient to provide physical support and structure to the associated polynucleotides present thereon under the assay conditions in which the array is employed, particularly under high throughput handling conditions.

The substrate may be biological, non-biological, organic, inorganic, or a combination of any of these, existing as particles, strands, precipitates, gels, sheets, tubing, spheres, containers, capillaries, pads, slices, films, plates, slides, etc. The substrate may have any convenient shape, such as a disc, square, sphere, circle, etc. The substrate is preferably flat or planar but may take on a variety of alternative surface configurations. The substrate may be a polymerized Langmuir Blodgett film, functionalized glass, Si, Ge, GaAs, GaP, SiO_2, SIN_4, modified silicon, or any one of a wide variety of gels or polymers such as (poly)tetrafluoroethylene, (poly)vinylidenedifluoride, polystyrene, polycarbonate, or combinations thereof. Other substrate materials will be readily apparent to those of skill in the art upon review of this disclosure.

In a preferred embodiment the substrate is flat glass or single-crystal silicon. According to some embodiments, the surface of the substrate is etched using well known techniques to provide for desired surface features. For example, by way of the formation of trenches, v-grooves, mesa structures, or the like, the synthesis regions may be more closely placed within the focus point of impinging light, be provided with reflective "mirror" structures for maximization of light collection from fluorescent sources, etc.

Surfaces on the solid substrate will usually, though not always, be composed of the same material as the substrate. Alternatively, the surface may be composed of any of a wide variety of materials, for example, polymers, plastics, resins, polysaccharides, silica or silica-based materials, carbon, metals, inorganic glasses, membranes, or any of the above-listed substrate materials. In some embodiments the surface may provide for the use of caged binding members which are attached firmly to the surface of the substrate. Preferably, the surface will contain reactive groups, which are carboxyl, amino, hydroxyl, or the like. Most preferably, the surface will be optically transparent and will have surface Si--OH functionalities, such as are found on silica surfaces.

The surface of the substrate is preferably provided with a layer of linker molecules, although it will be understood that the linker molecules are not required elements of the invention. The linker molecules are preferably of sufficient length to permit polynucleotides of the invention and on a substrate to hybridize to other polynucleotide molecules and to interact freely with molecules exposed to the substrate.

Often, the substrate is a silicon or glass surface, (poly)tetrafluoroethylene, (poly)vinylidendifluoride, polystyrene, polycarbonate, a charged membrane, such as nylon 66 or nitrocellulose, or combinations thereof. In a preferred embodiment, the solid support is glass. Preferably, at least one surface of the substrate will be substantially flat. Preferably, the surface of the solid support will contain reactive groups, including, but not limited to, carboxyl, amino, hydroxyl, thiol, or the like. In one embodiment, the surface is optically transparent. In a preferred embodiment, the substrate is a poly-lysine coated slide or Gamma amino propyl silane-coated Corning Microarray Technolgy-GAPS.

Any solid support to which a nucleic acid member may be attached may be used in the invention. Examples of suitable solid support materials include, but are not limited to, silicates

such as glass and silica gel, cellulose and nitrocellulose papers, nylon, polystyrene, polymethacrylate, latex, rubber, and fluorocarbon resins such as TEFLON™.

The solid support material may be used in a wide variety of shapes including, but not limited to slides and beads. Slides provide several functional advantages and thus are a preferred form of solid support. Due to their flat surface, probe and hybridization reagents are minimized using glass slides. Slides also enable the targeted application of reagents, are easy to keep at a constant temperature, are easy to wash and facilitate the direct visualization of RNA and/or DNA immobilized on the solid support. Removal of RNA and/or DNA immobilized on the solid support is also facilitated using slides.

The particular material selected as the solid support is not essential to the invention, as long as it provides the described function. Normally, those who make or use the invention will select the best commercially available material based upon the economics of cost and availability, the expected application requirements of the final product, and the demands of the overall manufacturing process.

Spotting method

The invention provides for arrays wherein each nucleic acid member comprising the array is spotted onto a solid support.

Preferably, spotting is carried out as follows. PCR products (~40 ul) of cDNA clones obtained from animals subjected to pain, in the same 96-well tubes used for amplification, are precipitated with 4 ul (1/10 volume) of 3M sodium acetate (pH 5.2) and 100 ul (2.5 volumes) of ethanol and stored overnight at –20°C. They are then centrifuged at 3,300 rpm at 4°C for 1 hour. The obtained pellets are washed with 50 ul ice-cold 70% ethanol and centrifuged again for 30 minutes. The pellets are then air-dried and resuspended well in 20ul 3X SSC overnight. The samples are then spotted, either singly or in duplicate, onto polylysine-coated slides (Sigma Cat. No. P0425) using a robotic GMS 417 arrayer (Affymetrix, CA).

The boundaries of the spots on the microarray are marked with a diamond scriber (note that the spots become invisible after post-processing). The arrays are rehydrated by suspending the slides over a dish of warm particle free ddH_20 for approximately one minute (the spots will swell slightly but will not run into each other) and snap-dried on a 70-80°C inverted heating block for 3 seconds. Nucleic acid is then UV crosslinked to the slide (Stratagene, Stratalinker,

65 mJ – set display to "650" which is 650 x 100 uJ). The arrays are placed in a slide rack. An empty slide chamber is prepared and filled with the following solution: 3.0 grams of succinic anhydride (Aldrich) was dissolved in 189 ml of 1-methyl-2-pyrrolidinone (rapid addition of reagent is crucial); immediately after the last flake of succinic anhydride is dissolved, 21.0 ml of 0.2 M sodium borate is mixed in and the solution is poured into the slide chamber. The slide rack is plunged rapidly and evenly in the slide chamber and vigorously shaken up and down for a few seconds, making sure the slides never leave the solution, and then mixed on an orbital shaker for 15-20 minutes. The slide rack is then gently plunged in 95°C ddH_20 for 2 minutes, followed by plunging five times in 95% ethanol. The slides are then air dried by allowing excess ethanol to drip onto paper towels. The arrays are then stored in the slide box at room temperature until use.

Numerous methods may be used for attachment of the nucleic acid members of the invention to the substrate (a process referred as spotting). For example, polynucleotides are attached using the techniques of, for example U.S. Pat. No. 5,807,522, which is incorporated herein by reference for teaching methods of polymer attachment.

Alternatively, spotting may be carried out using contact printing technology.

Kits

The invention provides for kits for performing expression assays using the pain-specific arrays of the present invention. Such kits according to the present invention will at least comprise the pain-specific arrays of the invention having associated differentially expressed nucleic acid members and packaging means therefore. The kits may further comprise one or more additional reagents employed in the various methods, such as: 1) primers for generating test polynucleotides; 2) dNTPs and/or rNTPs (either premixed or separate), optionally with one or more uniquely labeled dNTPs and/or rNTPs (e.g., biotinylated or Cy3 or Cy5 tagged dNTPs); 3) post synthesis labeling reagents, such as chemically active derivatives of fluorescent dyes; 4) enzymes, such as reverse transcriptases, DNA polymerases, and the like; 5) various buffer mediums, e.g., hybridization and washing buffers; 6) labeled probe purification reagents and components, like spin columns, etc.; and 7) signal generation and detection reagents, e.g., streptavidin-alkaline phosphatase conjugate, chemifluorescent or chemiluminescent substrate, and the like.

Therapeutic agents and Screening Methods

The present invention provides a number of potentially therapeutic compounds which may be used to modulate the expression of genes which are differentially expressed in an animal subjected to pain, or which may be used to modulate the activity of a protein encoded by a differentially expressed polynucleotide sequence of the invention, or which may be used to modulate pain in an animal. Such therapeutic agents include, but are not limited to a chemical compound, a protein, an antibody, RNAi, and an antisense nucleic acid. In a further aspect, the invention provides a method for screening potentially therapeutic agents for the ability to modulate the expression of genes which are differentially expressed in an animal subjected to pain, and further provides pharmaceutical formulations comprising the therapeutic agents. In a still further embodiment, the present invention provides a method of screening potentially therapeutic agents for the ability to modulate the activity of one or more polypeptides encoded by one or more of the polynucleotide sequences indicated in Tables 1, 2, 3, 4, or 5.

Therapeutic Agents

A therapeutic agent, useful in the present invention, changes (e.g., increases or decreases) the level of expression of at least one polynucleotide sequence that is differentially expressed in an animal subjected to pain. Preferably, a therapeutic agent causes a change in the level of expression of a polynucleotide sequence, that is, to increase or decrease the expression of a polynucleotide sequence that is differentially expressed in an animal subjected to pain, wherein the change results in the differentially expressed sequence being no longer differentially expressed by at least 1.4 fold (or differentially expressed by 1.2 fold in combination with a statistical significance of $p<0.05$ in at least three replicate assays) relative to the expression of the same sequence in a naïve animal.

In another embodiment, a therapeutic agent according to the invention can modulate the activity of one or more of the polypeptides specifically indicated in Tables 1, 2, 3, 4, or 5, or encoded by one or more of the polynucleotide sequences of Tables 1, 2, 3, 4, or 5.

In another embodiment, a therapeutic agent according to the invention can ameliorate at least one of the symptoms and/or physiological changes associated with pain including, but not limited to mechanical allodynia and hyperalgesia, and temperature allodynia and hyperalgesia.

The candidate therapeutic agent may be a synthetic compound, or a mixture of compounds, or may be a natural product (*e.g.* a plant extract or culture supernatant). According

to the invention, a therapeutic agent or compound can be a candidate or test compound. Similarly, according to the invention, a candidate or test compound can be a therapeutic agent.

Suitable test compounds for use in the screening assays of the invention can be obtained from any suitable source, e.g., conventional compound libraries. The test compounds can also be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds [Lam, (1997)]. Examples of methods for the synthesis of molecular libraries can be found in the art. Libraries of compounds may be presented in solution or on beads, bacteria, spores, plasmids or phage.

Candidate therapeutic agents or compounds from large libraries of synthetic or natural compounds may be screened as described below. Numerous means are currently used for random and directed synthesis of saccharide, peptide, and nucleic acid based compounds. Synthetic compound libraries are commercially available from a number of companies inclu Maybridge Chemical Co. (Trevillet, Cornwall, UK), Comgenex (Princeton, NJ), Brandon Associates (Merrimack, NH), and Microsource (New Milford, CT). A rare chemical library is available from Aldrich (Milwaukee, WI). Combinatorial libraries are available and are prepared. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available from e.g., Pan Laboratories (Bothell, WA) or MycoSearch (NC), or are readily produced by methods well known in the art. Additionally, natural and synthetically produced libraries and compounds are readily modified through conventional chemical, physical, and biochemical means.

Small Molecules

Useful compounds may be found within numerous chemical classes. Useful compounds may be organic compounds, or small organic compounds. Small organic compounds, or "small molecules" have a molecular weight of more than 50 yet less than about 2,500 daltons, preferably less than about 750, more preferably less than about 350 daltons. Exemplary classes include heterocycles, peptides, saccharides, steroids, and the like. Small molecules can be

nucleic acids, peptides, polypeptides, peptidomimetics, carbohydrates, lipids or other organic (carbon-containing) or inorganic molecules. The compounds may be modified to enhance efficacy, stability, pharmaceutical compatibility, and the like. Structural identification of an agent may be used to identify, generate, or screen additional agents. For example, where peptide agents are identified, they may be modified in a variety of ways to enhance their stability, such as using an unnatural amino acid, such as a D-amino acid, particularly D-alanine, by functionalizing the amino or carboxylic terminus, e.g. for the amino group, acylation or alkylation, and for the carboxyl group, esterification or amidification, or the like.

Antisense therapy

In one embodiment, a therapeutic agent, according to the invention, can be a differentially expressed nucleic acid or a sequence complementary thereto, useful in antisense therapy. The antisense sequence of a polynucletoide which is differentially expressed in an animal subjected to pain may be determined using the either the sequence indicated by accession number in tables 4-5, or the sequence of the rat and/or human differentially expressed sequences shown in Table 2-3 as set forth in the corresponding SEQ ID No. As used herein, antisense therapy refers to administration or *in situ* generation of oligonucleotide molecules or their derivatives which specifically hybridize (e.g., bind) under cellular conditions with the cellular mRNA and/or genomic DNA, thereby inhibiting transcription and/or translation of that gene. The binding may be by conventional base pair complementarity, or, for example, in the case of binding to DNA duplexes, through specific interactions in the major groove of the double helix. In general, antisense therapy refers to the range of techniques generally employed in the art, and includes any therapy which relies on specific binding to oligonucleotide sequences.

An antisense construct of the present invention can be delivered, for example, as an expression plasmid which, when transcribed in the cell, produces RNA which is complementary to at least a unique portion of the cellular mRNA identified as being differentially expressed in an animal subjected to pain. The construction and use of expression plasmids is described above and may be adapted by one of skill in the art to include expression plasmids or vectors comprising anitsense oligonucleotides. Alternatively, the antisense construct is an oligonucleotide probe which is generated ex vivo and which, when introduced into the cell, causes inhibition of expression by hybridizing with the mRNA and/or genomic sequences of a differentially expressed nucleic acid. Such oligonucleotide probes are preferably modified oligonucleotides which are resistant to endogenous nucleases, e.g., exonucleases and/or

endonucleases, and are therefore stable *in vivo*. Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphorothioate and methylphosphonate analogs of DNA (see also U.S. Patents 5,176,996; 5,264,564; and 5,256,775). Additionally, general approaches to constructing oligomers useful in antisense therapy have been reviewed, for example, by Van der Krol *et al.* (1988) BioTechniques 6:958-976; and Stein *et al.* (1988) Cancer Res 48:2659-2668. With respect to antisense DNA, oligodeoxyribonucleotides derived from the translation initiation site, e.g., between the -10 and +10 regions of the nucleotide sequence of interest, are preferred.

Antisense approaches involve the design of oligonucleotides (either DNA or RNA) that are complementary to mRNA (i.e., differentially expressed mRNA). The antisense oligonucleotides will bind to the mRNA transcripts and prevent translation. Absolute complementarity, although preferred, is not required. In the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

Oligonucleotides that are complementary to the 5' end of the differentially expressed mRNA, e.g., the 5' untranslated sequence up to and including the AUG initiation codon, should work most efficiently at inhibiting translation. However, sequences complementary to the 3' untranslated sequences of mRNAs have recently been shown to be effective at inhibiting translation of mRNAs as well. (Wagner, R. 1994. Nature 372:333). Therefore, oligonucleotides complementary to either the 5' or 3' untranslated, non-coding regions of a gene could be used in an antisense approach to inhibit translation of endogenous mRNA. Oligonucleotides complementary to the 5' untranslated region of the mRNA should include the complement of the AUG start codon. Antisense oligonucleotides complementary to mRNA coding regions are typically less efficient inhibitors of translation but could also be used in accordance with the invention. Whether designed to hybridize to the 5', 3', or coding region of subject mRNA, antisense nucleic acids should be at least six nucleotides in length, and are preferably less than about 100 and more preferably less than about 50, 25, 17 or 10 nucleotides in length.

The oligonucleotides can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors), or agents facilitating transport across the cell membrane (see, e.g., Letsinger *et al.*, 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre *et al.*, 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. WO 88/098 10, published December 15, 1988) or the blood-brain barrier (see, e.g., PCT Publication No. WO 89/10 134, published April 25, 1988), hybridization-triggered cleavage agents (See, e.g., Krol *et al.*, 1988, BioTechniques 6:958-976), or intercalating agents (See, e.g., Zon, 1988, Pharm. Res. 5:539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The antisense oligonucleotide may comprise at least one modified base moiety which is selected from the group including but not limited to 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xantine, 4-acetylcytosine, 5-(carboxyhydroxytriethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5- oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

The antisense oligonucleotide may also comprise at least one modified sugar moiety selected from the group including but not limited to arabinose, 2-fluoroarabinose, xylulose, and hexose.

The antisense oligonucleotide can also contain a neutral peptide-like backbone. Such molecules are termed peptide nucleic acid (PNA)-oligomers and are described, e.g., in Peny-O'Keefe *et al.* (1996) Proc. Natl. Acad. Sci. U.S.A. 93:14670 and in Eglom *et al.* (1993) Nature 365:566. One advantage of PNA oligomers is their capability to bind to complementary DNA

essentially independently from the ionic strength of the medium due to the neutral backbone of the DNA. In yet another embodiment, the antisense oligonucleotide comprises at least one modified phosphate backbone selected from the group consisting of a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methyiphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

In yet a further embodiment, the antisense oligonucleotide is an α-anomeric oligonucleotide. An α-anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual n-units, the strands run parallel to each other (Gautier *et al*, 1987, Nucl. Acids Res. 15:6625-6641). The oligonucleotide is a 2'-O-methylribonucleotide (Inoue *et al.*, 1987, Nucl. Acids Res. 15:6131-12148), or a chimeric RNA-DNA analogue (Jnoue *et al.*, 1987, FEBS Lett. 215:327-330).

Oligonucleotides of the invention may be synthesized by standard methods known in the art, e.g., by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.) based on the known sequence of the differentially expressed nucleic acid sequences. As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein *et al.* (1988, Nucl. Acids Res. 16:3209), methylphosphonate olgonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin *et al.*, 1988, Proc. Natl. Acad. Sci. U.S.A. 85:7448-7451), etc.

While antisense nucleotides complementary to a coding region sequence can be used, those complementary to the transcribed untranslated region and to the region comprising the initiating methionine are most preferred.

The antisense molecules can be delivered to cells which express the target nucleic acid *in vivo*. A number of methods have been developed for delivering antisense DNA or RNA to cells; e.g., antisense molecules can be injected directly into the tissue site, or modified antisense molecules, designed to target the desired cells (e.g., antisense linked to peptides or antibodies that specifically bind receptors or antigens expressed on the target cell surface) can be administered systemically.

However, it is often difficult to achieve intracellular concentrations of the antisense sufficient to suppress translation on endogenous mRNAs. Therefore, a preferred approach utilizes a recombinant DNA construct in which the antisense oligonucleotide is placed under the control of a strong pol III or pol II promoter. The use of such a construct to transfect target cells

in an animal will result in the transcription of sufficient amounts of single stranded RNAs that will form complementary base pairs with the endogenous transcripts and thereby prevent translation of the target mRNA. For example, a vector can be introduced *in vivo* such that it is taken up by a cell and directs the transcription of an antisense RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art, combined with those described above. Vectors can be plasmid, viral, or others known in the art for replication and expression in mammalian cells. Expression of the sequence encoding the antisense RNA can be by any promoter known in the art to act in animal, preferably mammalian cells. Such promoters can be inducible or constitutive. Such promoters include but are not limited to: the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290:304-3 10), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto *et al.*, 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner *et al.*, 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster et at, 1982, Nature 296:39-42), etc. Any type of plasmid, cosmid, YAC or viral vector can be used to prepare the recombinant DNA construct which can be introduced directly into the tissue site; e.g., the spinal cord, or dorsal root ganglion. Alternatively, viral vectors can be used which selectively infect the desired tissue (e.g., for brain, herpesvirus vectors may be used), in which case administration may be accomplished by another route (e.g., systemically).

Ribozymes

In another aspect of the invention, ribozyme molecules designed to catalytically cleave target mRNA transcripts can be used to prevent translation of target mRNA and expression of a target protein (See, e.g., PCT International Publication WO90/11364, published October 4, 1990; Sarver *et al.*, 1990, Science 247:1222-1225 and U.S. Patent No. 5,093,246). While ribozymes that cleave mRNA at site specific recognition sequences can be used to destroy target mRNAs, the use of hammerhead ribozymes is preferred. Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. The sole requirement is that the target mRNA have the following sequence of two bases: 5'-UG-3'. Ribozymes, useful in the present invention may be designed based on the known sequence of the nucleic acid sequence identified as being differentially expressed in an animal subjected to pain as described above. The construction and production of hammerhead

ribozymes is well known in the art and is described more fully in Haseloff and Gerlach, 1988, Nature, 334:585-591. Preferably the ribozyme is engineered so that the cleavage recognition site is located near the 5' end of the target mRNA; i.e., to increase efficiency and minimize the intracellular accumulation of non-functional mRNA transcripts.

The ribozymes of the present invention also include RNA endoribonucleases (hereinafter "Cech-type ribozymes") such as the one which occurs naturally in *Tetrahymena thermophila* (known as the IVS, or L-19 IVS RNA) and which has been extensively described by Thomas Cech and collaborators (Zaug, et al., 1984, Science, 224:574-578; Zaug and Cech, 1986, Science, 231:470-475; Zaug, et al., 1986, Nature, 324:429-433; published International patent application No. WO88/04300 by University Patents Inc.; Been and Cech, 1986, Cell, 47:207-216). The Cech-type ribozymes have an eight base pair active site which hybridizes to a target RNA sequence whereafter cleavage of the target RNA takes place. The invention encompasses those Cech-type ribozymes which target eight base-pair active site sequences that are present in a target gene.

As in the antisense approach, the ribozymes can be composed of modified oligonucleotides (e.g., for improved stability, targeting, etc.) and should be delivered to cells which express the target gene *in vivo*. A preferred method of delivery involves using a DNA construct "encoding" the ribozyme under the control of a strong constitutive pol III or pol II promoter, so that transfected cells will produce sufficient quantities of the ribozyme to destroy endogenous messages and inhibit translation. Because ribozymes, unlike antisense molecules, are catalytic, a lower intracellular concentration is required for efficiency.

Antisense RNA, DNA, and ribozyme molecules of the invention may be prepared by any method known in the art for the synthesis of DNA and RNA molecules. These include techniques for chemically synthesizing oligodeoxyribonucleotides and oligoribonucleotides well known in the art such as for example solid phase phosphoramidite chemical synthesis. The sequences of the antisense and ribozyme molecules will be based on the known sequence of the differentially expressed nucleic acid molecules. Alternatively, RNA molecules may be generated by *in vitro* and *in vivo* transcription of DNA sequences encoding the antisense RNA molecule. Such DNA sequences may be incorporated into a wide variety of vectors which incorporate suitable RNA polymerase promoters such as the T7 or SP6 polymerase promoters. Alternatively, antisense cDNA constructs that synthesize antisense RNA constitutively or inducibly, depending on the promoter used, can be introduced stably into cell lines.

Moreover, various well-known modifications to nucleic acid molecules may be introduced as a means of increasing intracellular stability and half-life. Possible modifications include but are not limited to the addition of flanking sequences of ribonucleotides or deoxyribonucleotides to the 5' and/or 3' ends of the molecule or the use of phosphorothioate or 2' 0-methyl rather than phosphodiesterase linkages within the oligodeoxyribonucleotide backbone.

RNAi therapy

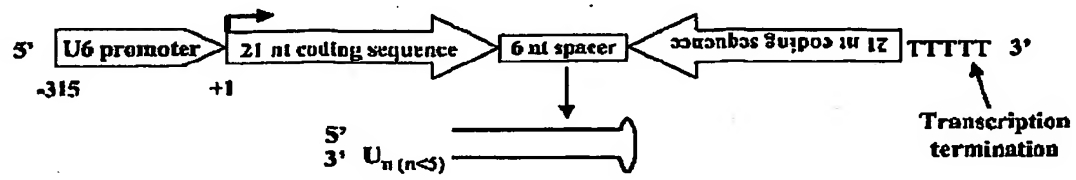
In another embodiment, a therapeutic agent according to the invention can be a double stranded RNAi molecule that is specifically targeted to one or more of the polynucleotide sequences which are differentially expressed in an animal subjected to pain relative to an animal that is not subjected to pain (see Tables 1, 2, 3, 4, or 5). As used herein, RNAi or RNA interference refers to the gene-specific, double stranded RNA (dsRNA) mediated, post-transcriptional silencing of gene expression as described in the review by Hannon, G., (2002) Nature 418, 244-250, which is herein incorporated in its entirety. Current experimental evidence indicates that RNAis specific for a target RNA are recognized and processed into 21 and 23 nucleotide small interfering RNAs (siRNAs) by the Dicer RNase III endonuclease. SiRNAs are then incorporated into a RNA induced silencing complex (RISC) which becomes activated by unwinding of the duplex siRNA. Activated RISC complexes then promote RNA degradation and translation inhibition of the target RNA.

In mammals, RNAi therapy, according to the invention, refers to gene-specific suppression that can be achieved by generating siRNA (Elbashir, S. M. et al. (2001) Nature (London) 411, 494–498). *In vitro* synthesized siRNAs can be prepared by any method known in the art for the synthesis of RNA molecules. These include techniques for chemically synthesizing oligoribonucleotides that are well known in the art, for example, solid phase phosphoramidite chemical synthesis. The sequences of the siRNA molecules are based on the known sequence of the differentially expressed nucleic acid molecules. Alternatively, siRNA molecules can be generated by the T7 or SP6 polymerase promoter driven *in vitro* transcription of DNA sequences encoding the siRNA molecule. *In vitro* synthesized siRNAs can be delivered to cells either by direct injection of *in vitro* synthesized siRNAs into the tissue site. Alternatively, modified siRNAs, designed to target the desired cells (via linkage to peptides or antibodies that specifically bind to cell surface receptors or antigens), can be administered systemically.

In a preferred embodiment, the siRNAs of the invention are delivered to a target cell as an expression plasmid under the control of a RNA polymerase II or III promoter. When transcribed in the cell, siRNA is generated which is complementary to a cellular mRNA identified as being differentially expressed in an animal subjected to pain. The construction and use of expression plasmids is described above and may be adapted by one of skill in the art to include siRNA expression plasmids. Such vectors can be constructed by recombinant DNA technology methods standard in the art, combined with those described above. Vectors can be plasmid, viral, or others known in the art for replication and expression in mammalian cells. Expression of the sequence encoding the siRNA can be by any promoter known in the art to act in an animal, preferably mammalian cells. Such promoters can be inducible or constitutive. Such promoters include but are not limited to: the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290:304-3 10), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto *et al.*, 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner *et al.*, 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster et at, 1982, Nature 296:39-42), etc as well as neural specific promoters, for example the nestin promoter. Any plasmid, cosmid, YAC or viral vector can be used to prepare the recombinant DNA construct which can be introduced directly into the tissue site; e.g., the spinal cord, or dorsal root ganglion. Alternatively, viral vectors can be used which selectively infect the desired tissue (e.g., for brain, herpes virus vectors may be used), in which case administration may be accomplished by another route (e.g., systemically).

In a preferred embodiment, the siRNA expression vectors of the invention are synthesized from a DNA template under the control of an RNA polymerase III (Pol III) promoter in transfected cells or transgenic animals (see below). Pol III directs the synthesis of small, noncoding transcripts whose 3' ends are defined by termination within a stretch of 4–5 thymidines (Ts) (Sui et al. PNAS (2002) vol. 99, 5515–5520). Addition of 3' overhangs contributes to the activity of siRNA synthesized *in vitro* (Elbashir, S. M et al. (2001) *Genes Dev.* 15, 188–200). Transfection of such a construct into target cells results in the transcription of sufficient amounts of siRNAs to base pair with the endogenous transcripts, promote its degradation and thereby prevent translation of the target mRNA. The vector can remain episomal or become chromosomally integrated. Alternatively the construct may be incorporated into a viral vector such as herpes virus vectors as described *supra*.

An example of a mouse U6 pol III transcribed siRNA expression plasmid is shown below where the 21 nucleotide sequence is specific for one or more of the differentially expressed sequences shown in Tables 1, 2, 3, 4, or 5 (see Sui et al. PNAS (2002) vol. 99, 5515–5520):



Supplemental therapy

The differentially expressed nucleic acid sequences described herein may exhibit either increased or decreased expression. The antisense methods described above are directed primarily at inhibiting the expression of a differentially overexpressed sequence. Alternatively, in the situation where differential expression is manifested in a decrease in sequence expression, the underexpressed sequence may be supplied to the animal in an expression vector as described above. If for example, through the process of identifying and verifying the differential expression of nucleic acid sequences obtained from an animal subjected to pain, a sequence is identified which is expressed at a level at least 1.2 fold less than in a naïve animal in at least three replicate analyses with a significance of $p<0.05$ (or, alternatively, at least 1.4 fold less), the sequence may be cloned into a suitable expression vector for expression of the sequence in the animal subjected to pain. Either viral or non-viral gene delivery methods may be used to introduce the construct into the animal cells as described above. Briefly, the deficient sequence may be cloned into any expression vector known in the art which is compatible with the animal cell into which it is intended to be introduced, and which is capable of supporting expression of the recombinant sequence. The vector used may be chosen to replicate episomaly or may integrate in the cell chromosome, provided that either mode of replication permits the expression of the deficient nucleic acid sequence. Further, any promoter sequence which is sufficient to direct expression of the recombinant sequence may be used in the vector to direct expression of the sequence. In a preferred embodiment, the promoter is constitutively active in the animal, given that the goal is to attain a level of gene expression sufficient to replace the deficiently expressed sequence. In a further preferred embodiment, the promoter is a neuron-specific promoter. Vectors comprising the deficient sequence may be introduced into cells of the animal

subjected to pain using any technique known to those of skill in the art, including, but not limited to microinjection and viral delivery.

Similarly, those proteins which are encoded by polynucleotide sequences which are differentially expressed as indicated in Tables 1, 2, 3, 4, or 5, and which are also indicated in the column labeled "subcellular localization" (i.e., in Table 2) as being a secreted protein, may be screened for their ability to modulate the activity of one or more of the proteins indicated in Tables 1, 2, 3, 4, or 5, or screened for their ability to modulate pain in an animal.

Once a therapeutic gene is defined, whether it be an antisense molecule, ribozyme, or supplemental sequence, the gene sequence is subcloned into a vector suitable for the purpose of gene therapy. Murine leukemia virus (MLV)-based retroviral vectors are one of the most widely used gene delivery vehicles in gene therapy clinical trials and have been employed in almost 70% of approved protocols (Ali, M. et al., *Gene Ther.*, 1:367-384, 1994; Marshall, E., *Science*, 269:1050-1055, 1995). Other useful vectors are also known in the art (e.g., Carter and Samulski, 2000, *Int. J. Mol. Med.* 6:17-27; Lever et al., 1999, *Biochem. Soc. Trans.* 27: 841-7). Methods for gene therapy of human diseases are described in U.S. Patent Nos. 6,190,907; 6,187,305; 6,140,087; and 6,129,705.

Screening Assays

Protein Activity Regulators

Regulators as used herein, refer to compounds that affect the activity of a "differentially expressed protein" in vivo and/or in vitro. As used herein, the term "differentially expressed protein (or polypeptide)" will refer to the proteins of Table 1, 2, 3, 4, or 5 that are encoded by sequences that are differentially expressed in pain. Regulators can be agonists and antagonists of a differentially expressed polypeptide and can be compounds that exert their effect on the differentially expressed protein activity via the enzymatic activity, expression, post-translational modifications or by other means. Agonists of a differentially expressed protein are molecules which, when bound to a differentially expressed protein, increase or prolong the activity of a differentially expressed protein. Agonists of a differentially expressed protein include proteins, nucleic acids, carbohydrates, small molecules, or any other molecule which activate a differentially expressed protein. Antagonists of a differentially expressed protein are molecules which, when bound to a differentially expressed protein, decrease the amount or the duration of the activity of a differentially expressed protein. Antagonists include proteins, nucleic acids,

carbohydrates, antibodies, small molecules, or any other molecule which decrease the activity of a "differentially expressed protein". The activity of a differentially expressed protein, useful in the present invention is indicated in Table 2, 3, 4, or 5 either directly in columns labeled "identifier", "description" and/or "protein type", or may be inferred from the information provided in the column labeled "subcellular localization" (Table 2). For example, if a protein is localized to the cell membrane, then one of skill in the art would be able to determine that the activity of such a protein would be that of a receptor, for example, or an ion channel, and screen candidate compounds against this protein activity accordingly.

The term "modulate", as it appears herein, refers to a change in the activity of a differentially expressed protein. For example, modulation may cause an increase or a decrease in enzymatic activity, binding characteristics, or any other biological, functional, or immunological properties of a differentially expressed protein.

As used herein, the terms "specific binding" or "specifically binding" refer to that interaction between a protein or peptide and an agonist, an antibody, or an antagonist. The interaction is dependent upon the presence of a particular structure of the protein recognized by the binding molecule (i.e., the antigenic determinant or epitope). For example, if an antibody is specific for epitope "A" the presence of a polypeptide containing the epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

The invention provides methods (also referred to herein as "screening assays") for identifying compounds which can be used for the treatment of pain. The methods entail the identification of candidate or test compounds or agents (e.g., peptides, peptidomimetics, small molecules or other molecules) which bind to a differentially expressed protein and/or have a stimulatory or inhibitory effect on the biological activity of a differentially expressed protein or its expression and then determining which of these compounds have an effect on pain symptoms in an in vivo assay.

Candidate or test compounds or agents which bind to a differentially expressed protein and/or have a stimulatory or inhibitory effect on the activity or the expression of a differentially expressed protein are identified either in assays that employ cells which express a differentially expressed protein (cell-based assays) or in assays with an isolated differentially expressed protein (cell-free assays). The various assays can employ a variety of variants of a differentially

expressed protein (e.g., full-length differentially expressed protein, a biologically active fragment of a differentially expressed protein, or a fusion protein which includes all or a portion of a differentially expressed protein). Moreover, a differentially expressed protein can be derived from any suitable mammalian species (e.g., human differentially expressed protein, rat differentially expressed protein or murine differentially expressed protein). The assay can be a binding assay entailing direct or indirect measurement of the binding of a test compound or a known differentially expressed protein ligand to a differentially expressed protein. The assay can also be an activity assay entailing direct or indirect measurement of the activity of a differentially expressed protein. The assay can also be an expression assay entailing direct or indirect measurement of the expression of a differentially expressed protein mRNA or a differentially expressed protein. The various screening assays are combined with an in vivo assay entailing measuring the effect of the test compound on the pain symtoms.

In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of a membrane-bound (cell surface expressed) form of the differentially expressed protein. Such assays can employ the full-length differentially expressed protein, a biologically active fragment of the differentially expressed protein, or a fusion protein which includes all or a portion of the differentially expressed protein. As described in greater detail below, the test compound can be obtained by any suitable means, e.g., from conventional compound libraries. Determining the ability of the test compound to bind to a membrane-bound form of the differentially expressed protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the differentially expressed protein-expressing cell can be measured by detecting the labeled compound in a complex. For example, the test compound can be labelled with ^{125}I, ^{35}S, ^{14}C, or ^{3}H, either directly or indirectly, and the radioisotope detected by direct counting of radioemmission or by scintillation counting. Alternatively, the test compound can be enzymatically labelled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product.

In a competitive binding format, the assay comprises contacting the differentially expressed protein-expressing cell with a known compound which binds to the differentially expressed protein to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with the differentially expressed

protein-expressing cell, wherein determining the ability of the test compound to interact with the differentially expressed protein-expressing cell comprises determining the ability of the test compound to preferentially bind the differentially expressed protein expressing cell as compared to the known compound.

In another embodiment, the assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of the differentially expressed protein (e.g., full-length differentially expressed protein, a biologically active fragment of the differentially expressed protein , or a fusion protein which includes all or a portion of the differentially expressed protein) expressed on the cell surface with a test compound and determining the ability of the test compound to modulate (e.g., stimulate or inhibit) the activity of the membrane-bound form of the differentially expressed protein. Determining the ability of the test compound to modulate the activity of the membrane-bound form of the differentially expressed protein can be accomplished by any method suitable for measuring the activity of the differentially expressed protein , e.g., any method suitable for measuring the activity of a G-protein coupled receptor or other seven-transmembrane receptor (described in greater detail below). The activity of a seven-transmembrane receptor can be measured in a number of ways, not all of which are suitable for any given receptor. Among the measures of activity are: alteration in intracellular Ca2+ concentration, activation of phospholipase C, alteration in intracellular inositol triphosphate (IP3) concentration, alteration in intracellular diacylglycerol (DAG) concentration, and alteration in intracellular adenosine cyclic 3', 5'-monophosphate (cAMP) concentration.

The present invention includes biochemical, cell free assays that allow the identification of inhibitors and agonists of phosphodiesterases (PDEs) suitable as lead structures for pharmacological drug development. Such assays involve contacting a form of a differentially expressed protein (e.g., full-length differentially expressed protein, a biologically active fragment of a differentially expressed protein, or a fusion protein comprising all or a portion of a differentially expressed protein) with a test compound and determining the ability of the test compound to act as an antagonist (preferably) or an agonist of the enzymatic activity of a differentially expressed protein. In one embodiment, the assay includes monitoring the PDE activity of a differentially expressed protein by measuring the conversion of either cAMP or cGMP to its nucleoside monophosphate after contacting a differentially expressed protein with a test compound.

For example, cAMP and cGMP levels can be measured by the use of the tritium containing compounds 3HcAMP and 3HcGMP as described in [Hansen, R.S., and Beavo, J.A., PNAS USA1982;79: 2788-92]. To screen a compound pool comprised of a large number of compounds, the microtiter plate-based scintillation proximity assay (SPA) as described in [Bardelle, C. et al. (1999) Anal. Biochem. 275: 148-155] can be applied.

Alternatively, the phosphodiesterase activity of the recombinant protein can be assayed using a commercially available SPA kit (Amersham Pharmacia). The PDE enzyme hydrolyzes cyclic nucleotides, e.g. cAMP and cGMP to their linear counterparts. The SPA assay utilizes the tritiated cyclic nucleotides [3H]cAMP or [3H]cGMP, and is based upon the selective interaction of the tritiated non cyclic product with the SPA beads whereas the cyclic substrates are not effectively binding. Radiolabelled product bound to the scintillation beads generates light that can be analyzed in a scintillation counter.

The cell-free assays of the present invention are amenable to use of either a membrane-bound form of the differentially expressed protein or a soluble fragment thereof. In the case of cell-free assays comprising the membrane-bound form of the polypeptide, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of the polypeptide is maintained in solution. Examples of such solubilizing agents include, but are not limited to ,non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton X-100, Triton X-114, Thesit, Iso-tri-decy-poly-(ethylene glycol ether)n, 3-[(3-cholamidopropyl)dimethylamminio]-1-propane sulfonate (CHAPS), 3-[(3-cholamidopropyl)dimethylamminio]-2-hydroxy-1-propane sulfonate (CHAPSO), or N-dodecyl=N,N-dimethyl-3-ammonio-1-propane sulfonate.

In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of a differentially expressed protein. Such assays can employ full-length differentially expressed protein, a biologically active fragment of a differentially expressed protein, or a fusion protein which includes all or a portion of a differentially expressed protein. As described in greater detail below, the test compound can be obtained by any suitable means, e.g., from conventional compound libraries.

Determining the ability of the test compound to modulate the activity of a differentially expressed protein can be accomplished, for example, by determining the ability of a differentially expressed protein to bind to or interact with a target molecule. The target molecule

can be a molecule with which a differentially expressed protein binds or interacts with in nature. The target molecule can be a component of a signal transduction pathway which facilitates transduction of an extracellular signal. The target differentially expressed protein molecule can be, for example, a second intracellular protein which has catalytic activity or a protein which facilitates the association of downstream signaling molecules with a differentially expressed protein.

Determining the ability of a differentially expressed protein to bind to or interact with a target molecule can be accomplished by one of the methods described above for determining direct binding. In one embodiment, determining the ability of a polypeptide of the invention to bind to or interact with a target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (e.g., intracellular Ca2+, diacylglycerol, IP3, etc.), detecting catalytic/enzymatic activity of the target on an appropriate substrate, detecting the induction of a reporter gene (e.g., a regulatory element that is responsive to a polypeptide of the invention operably linked to a nucleic acid encoding a detectable marker, e.g., luciferase), or detecting a cellular response.

In various embodiments of the above assay methods of the present invention, it may be desirable to immobilize a differentially expressed protein (or a differentially expressed protein target molecule) to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to a differentially expressed protein, or interaction of a differentially expressed protein with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtitre plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided which adds a domain that allows one or both of the proteins to be bound to a matrix. For example, glutathione-S-transferase (GST) fusion proteins or glutathione-S-transferase fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical; St. Louis, Mo.) or glutathione derivatized microtitre plates, which are then combined with the test compound or the test compound and either the non-adsorbed target protein or a differentially expressed protein, and the mixture incubated under conditions conducive to complex formation (e.g., at physiological conditions for salt and pH). Following incubation, the beads or microtitre plate wells are washed to remove any unbound components and complex formation is measured either

directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of binding or activity of a differentially expressed protein can be determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either a differentially expressed protein or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated polypeptide of the invention or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the art (e.g., biotinylation kit, Pierce Chemicals; Rockford, Ill.), and immobilized in the wells of streptavidin-coated plates (Pierce Chemical). Alternatively, antibodies reactive with a differentially expressed protein or target molecules but which do not interfere with binding of the polypeptide of the invention to its target molecule can be derivatized to the wells of the plate, and unbound target or polypeptide of the invention trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immuno-detection of complexes using antibodies reactive with a differentially expressed protein or target molecule, as well as enzyme-linked assays which rely on detecting an enzymatic activity associated with a differentially expressed protein or target molecule.

Another technique for drug screening which may be used provides for high throughput screening of compounds having suitable binding affinity to the protein of interest as described in published PCT application WO84/03564. In this method, large numbers of different small test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. The test compounds are reacted with a differentially expressed protein, or fragments thereof, and washed. Bound differentially expressed protein is then detected by methods well known in the art. Purified differentially expressed protein can also be coated directly onto plates for use in the afore-mentioned drug screening techniques. Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding differentially expressed protein specifically compete with a testcompound for binding a differentially expressed protein. In this manner, antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with a differentially expressed protein.

The screening assay can also involve monitoring the expression of a differentially expressed protein. For example, regulators of expression of a differentially expressed protein can be identified in a method in which a cell is contacted with a candidate compound and the expression of a differentially expressed protein protein or mRNA in the cell is determined. The level of expression of a differentially expressed protein or mRNA the presence of the candidate compound is compared to the level of expression of a differentially expressed protein or mRNA in the absence of the candidate compound. The candidate compound can then be identified as a regulator of expression of a differentially expressed protein based on this comparison. For example, when expression of a differentially expressed protein or mRNA protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of a differentially expressed protein or mRNA expression. Alternatively, when expression of a differentially expressed protein or mRNA is less (statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of a differentially expressed protein or mRNA expression. The level of a differentially expressed protein or mRNA expression in the cells can be determined by methods described below.

Screening for therapeutic agents using Binding Assays

For binding assays, the test compound is preferably a small molecule which binds to and occupies the active site of a differentially expressed protein polypeptide, thereby making the ligand binding site inaccessible to substrate such that normal biological activity is prevented. Examples of such small molecules include, but are not limited to, small peptides or peptide-like molecules. Potential ligands which bind to a polypeptide of the invention include, but are not limited to, the natural ligands of known differentially expressed protein PDEs and analogues or derivatives thereof.

In binding assays, either the test compound or the differentially expressed polypeptide can comprise a detectable label, such as a fluorescent, radioisotopic, chemiluminescent, or enzymatic label, such as horseradish peroxidase, alkaline phosphatase, or luciferase. Detection of a test compound which is bound to differentially expressed polypeptide can then be accomplished, for example, by direct counting of radioemmission, by scintillation counting, or by determining conversion of an appropriate substrate to a detectable product. Alternatively, binding of a test compound to a differentially expressed polypeptide can be determined without labeling either of the interactants. For example, a microphysiometer can be used to detect

binding of a test compound with a differentially expressed polypeptide. A microphysiometer (e.g., Cytosensor™) is an analytical instrument that measures the rate at which a cell acidifies its environment using a light-addressable potentiometric sensor (LAPS). Changes in this acidification rate can be used as an indicator of the interaction between a test compound and a differentially expressed protein [Haseloff, (1988)].

Determining the ability of a test compound to bind to differentially expressed protein also can be accomplished using a technology such as real-time Bimolecular Interaction Analysis (BIA) [McConnell, (1992); Sjolander, (1991)]. BIA is a technology for studying biospecific interactions in real time, without labeling any of the interactants (e.g., BIAcoreTM). Changes in the optical phenomenon surface plasmon resonance (SPR) can be used as an indication of real-time reactions between biological molecules.

In yet another aspect of the invention, a differentially expressed protein-like polypeptide can be used as a "bait protein" in a two-hybrid assay or three-hybrid assay [Szabo, (1995); U.S. 5,283,317), to identify other proteins which bind to or interact with a differentially expressed protein and modulate its activity.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. For example, in one construct, polynucleotide encoding a differentially expressed protein can be fused to a polynucleotide encoding the DNA binding domain of a known transcription factor (e.g., GAL-4). In the other construct a DNA sequence that encodes an unidentified protein ("prey" or "sample") can be fused to a polynucleotide that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact in vivo to form an protein-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows tran-scription of a reporter gene (e.g., LacZ), which is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected, and cell colonies containing the functional transcription factor can be isolated and used to obtain the DNA sequence encoding the protein which interacts with a differentially expressed protein.

It may be desirable to immobilize either the differentially expressed protein (or polynucleotide) or the test compound to facilitate separation of the bound form from unbound

forms of one or both of the interactants, as well as to accommodate automation of the assay. Thus, either the differentially expressed protein-like polypeptide (or polynucleotide) or the test compound can be bound to a solid support. Suitable solid supports include, but are not limited to, glass or plastic slides, tissue culture plates, microtiter wells, tubes, silicon chips, or particles such as beads (including, but not limited to, latex, polystyrene, or glass beads). Any method known in the art can be used to attach the differentially expressed protein-like polypeptide (or polynucleotide) or test compound to a solid support, including use of covalent and non-covalent linkages, passive absorption, or pairs of binding moieties attached respectively to the polypeptide (or polynucleotide) or test compound and the solid support. Test compounds are preferably bound to the solid support in an array, so that the location of individual test compounds can be tracked. Binding of a test compound to the differentially expressed protein (or a polynucleotide encoding for the differentially expressed protein) can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and microcentrifuge tubes.

In one embodiment, the differentially expressed protein is a fusion protein comprising a domain that allows binding of the differentially expressed protein to a solid support. For example, glutathione-S-transferase fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, Mo.) or glutathione derivatized microtiter plates, which are then combined with the test compound or the test compound and the non-adsorbed differentially expressed protein; the mixture is then incubated under conditions conducive to complex formation (e.g., at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components. Binding of the interactants can be determined either directly or indirectly, as described above. Alternatively, the complexes can be dissociated from the solid support before binding is determined.

Other techniques for immobilizing proteins or polynucleotides on a solid support also can be used in the screening assays of the invention. For example, either the differentially expressed protein (or a polynucleotide encoding the differentially expressed protein) or a test com-pound can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated differentially expressed protein (or a polynucleotide encoding biotinylated differentially expressed protein) or test compounds can be prepared from biotin-NHS (N-hydroxysuccinimide) using techniques well known in the art (e.g., biotinylation kit, Pierce Chemicals, Rockford, Ill.) and immobilized in the wells of streptavidin-coated plates (Pierce Chemical). Alternatively, antibodies which

specifically bind to the differentially expressed protein, polynucleotide, or a test compound, but which do not interfere with a desired binding site, such as the active site of the differentially expressed protein, can be derivatized to the wells of the plate. Unbound target or protein can be trapped in the wells by antibody conjugation.

Methods for detecting such complexes; in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies which specifically bind to the differentially expressed protein or test compound, enzyme-linked assays which rely on detecting an activity of the differentially expressed protein, and SDS gel electrophoresis under non-reducing conditions.

Screening for test compounds which bind to the differentially expressed protein or polynucleotide also can be carried out in an intact cell. Any cell which comprises the differentially expressed polypeptide or polynucleotide can be used in a cell-based assay system. A differentially expressed protein polynucleotide can be naturally occurring in the cell or can be introduced using techniques such as those described above. Binding of the test compound to the differentially expressed protein or a polynucleotide encoding the differentially expressed protein is determined as described above.

Functional Assays

Test compounds can be tested for the ability to increase or decrease activity of a differentially expressed polypeptide. The differentially expressed protein activity can be measured, for example, using methods described in the specific examples, below. differentially expressed protein activity can be measured after contacting either a purified differentially expressed protein or an intact cell with a test compound. A test compound which decreases the differentially expressed protein activity by at least about 10, preferably about 50, more preferably about 75, 90, or 100% is identified as a potential agent for decreasing the differentially expressed protein activity. A test compound which increases the differentially expressed protein activity by at least about 10, preferably about 50, more preferably about 75, 90, or 100% is identified as a potential agent for increasing the differentially expressed protein activity.

Gene Expression

In another embodiment, test compounds which increase or decrease the differentially expressed protein gene expression are identified (i.e., test compounds which increase or decrease the expression of a differentially expressed polynucleotide sequence of the invention). As used herein, the term "correlates with expression of a poly-nucleotide" indicates that the detection of the presence of nucleic acids, the same or related to a nucleic acid sequence encoding the differentially expressed protein, by northern analysis or realtime PCR is indicative of the presence of nucleic acids encoding the differentially expressed protein in a sample, and thereby correlates with expression of the transcript from the polynucleotide encoding the differentially expressed protein. The term "microarray", as used herein, refers to an array of distinct polynucleotides or oligonucleotides arrayed on a substrate, such as paper, nylon or any other type of membrane, filter, chip, glass slide, or any other suitable solid support. A differentially expressed protein polynucleotide is contacted with a test compound, and the expression of an RNA or polypeptide product of the differentially expressed protein polynucleotide is determined. The level of expression of appropriate mRNA or polypeptide in the presence of the test compound is compared to the level of expression of mRNA or polypeptide in the absence of the test compound. The test compound can then be identified as a regulator of expression based on this comparison. For example, when expression of mRNA or polypeptide is greater in the presence of the test compound than in its absence, the test compound is identified as a stimulator or enhancer of the mRNA or polypeptide expression. Alternatively, when expression of the mRNA or polypeptide is less in the presence of the test compound than in its absence, the test compound is identified as an inhibitor of the mRNA or polypeptide expression.

The level of the differentially expressed protein mRNA or polypeptide expression in the cells can be determined by methods well known in the art for detecting mRNA or polypeptide. Either qualitative or quantitative methods can be used. The presence of polypeptide products of the differentially expressed protein polynucleotide can be determined, for example, using a variety of techniques known in the art, including immunochemical methods such as radioimmunoassay, Western blotting, and immunohistochemistry. Alternatively, polypeptide synthesis can be determined in vivo, in a cell culture, or in an in vitro translation system by detecting incorporation of labelled amino acids into the differentially expressed protein.

Such screening can be carried out either in a cell-free assay system or in an intact cell. Any cell which expresses the differentially expressed protein polynucleotide can be used in a cell-based assay system. The the differentially expressed protein polynucleotide can be naturally

occurring in the cell or can be introduced using techniques such as those described above. Either a primary culture or an established cell line can be used.

Screening of therapeutic agents against pain-specific array

In one embodiment the present invention provides a method for screening agents for their ability to regulate the expression of genes which are differentially expressed in an animal subjected to pain. In brief, the method comprises administering to an animal subjected to pain, such as an animal pain model, a potentially therapeutic agent, isolating nucleic acid from sensory neurons of the animal, preparing the nucleic acid for hybridization to a microarray as described above, and hybridizing the nucleic acid to a pain-specific microarray. The hybridization level is then compared to the hybridization of a nucleic acid sample contacted with the pain-specific microarray obtained from an animal subjected to pain, but not administered the potentially therapeutic agent. In one embodiment, the potentially therapeutic agent is deemed to be therapeutic if the expression level of the nucleic acid sequence obtained from the animal subjected to pain and treated with the agent is no longer differentially expressed by at least 1.4 fold, and wherein the expression of the nucleic acid sequence obtained from the animal subjected to pain but not treated with the agent remains differentially regulated. The nucleic acid sequences analyzed to determine therapeutic efficacy can include any of the sequences previously identified (see above) as being differentially expressed in an animal subjected to pain.

Animals may be administered any potentially therapeutic agent known in the art, including antisense molecules, ribozymes, and supplemental nucleic acid sequences as described above. Additional therapeutic agents include any agent known in the art which is routinely administered for the amelioration of pain including, but not limited to asprin, ibuprofen, narcotics, steroidial and non-steroidial anti-inflammatories, and the like. These agents are administered according to dosing protocols well known in the art.

Screening of therapeutic agents against individual genes that are differentially expressed in pain

Candidate therapeutic agents of the invention are screened for their ability to regulate the expression of one or more isolated polynucleotide sequences which have been identified herein as differentially regulated in an animal which has been subjected to pain relative to an animal that is not subjected to pain. In one embodiment, the screen consists of administering a candidate therapeutic agent, as defined herein, or a placebo, to an animal that is subjected to pain and

hybridizing a nucleic acid sample, corresponding to RNA obtained from such a treated or non treated animal, to a probe specific for a polynucleotide sequence selected from the group of isolated polynucleotide sequences of Tables 1, 2, 3, 4, or 5. In another embodiment, the screen consists of administering a candidate therapeutic agent, as defined herein, or a placebo, to an *in vitro* cell culture of primary cells for example, primary neurons, that naturally express polynucleotide sequences selected from the group of isolated polynucleotide sequences of Tables 1, 2, 3, 4, or 5. In a further embodiment, the screen consists of administering a candidate therapeutic agent, as defined herein, or a placebo, to cell lines that have been transfected with vectors that direct the expression of polynucleotide sequences selected from the group of isolated polynucleotide sequences of Tables 1, 2, 3, 4, or 5. In a further embodiment, the screen consists of administering a candidate therapeutic agent, as defined herein, or a placebo, to a transgenic animal in which a neural specific promoter drives the expression of a polynucleotide sequence selected from the group of isolated polynucleotide sequences of Tables 1, 2, 3, 4, or 5. In all instances, a 10% increase or decrease in the differential expression of a gene in response to a therapeutic compound is indicative of a therapeutic agent that can modulate the differential expression of a gene that is differentially regulated in an animal which has been subjected to pain relative to an animal that is not subjected to pain. In a preferred embodiment, nucleic acid samples obtained from treated and non-treated animals or *in vitro* cell cultures are hybridized to 1 or more, 2 or more, 5 or more, 50 or more, 100 or more, 500 or more, 1000 or more probes, each probe being specific to a polynucleotide sequence selected from the group of differentially expressed polynucleotide sequences of Tables 1, 2, 3, 4, or 5.

Methods for measuring the differential expression of one or more of the polynucleotides sequences of Tables 1, 2, 3, 4, or 5 in nucleic acid samples from treated animals relative to non-treated animals, are well known in the art and include, but are not limited to, reverse transcription PCR (RT-PCR; described in U.S. Patent No. 5,4078,00), Taqman (as disclosed in U.S. Patent Nos. 5,210,015 and 5,487,972), Molecular Beacon assays (as disclosed in WO 95/13399), Northern blot hybridization, S1 nuclease mapping, RNAse protection assays which are described in the literature. See, e.g., Sambrook, Fritsch & Maniatis, 1989, Molecular Cloning: A Laboratory Manual, Second Edition ; Oligonucleotide Synthesis (M.J. Gait, ed., 1984); Nucleic Acid Hybridization (B.D. Harnes & S.J. Higgins, eds., 1984); A Practical Guide to Molecular Cloning (B. Perbal, 1984); and a series, Methods in Enzymology (Academic Press, Inc.); Short Protocols In Molecular Biology, (Ausubel et al., ed., 1995). References to patents and literature are by incorporated in their entirety.

Compounds identified as positives based on this screen can be further tested for activity in the *in vitro* cell culture assay, *in vivo* protein activity assay or analgesic assays, described herein, to determine if these compounds are effective at modulating differential gene expression in response to pain and ultimately attenuating pain itself.

Polypeptide Activity

In one embodiment, the present invention provides a method for screening potentially therapeutic agents which modulate the activity of one or more polypeptides encoded by one or more of the polynucleotide sequences in Tables 1, 2, 3, 4, or 5, such that if the activity of the polypeptide is increased in an animal subjected to pain, the therapeutic substance will decrease the activity of the polypeptide relative to the activity of the same polypeptide in an animal subjected to pain, but not treated with the therapeutic agent. Likewise, if the activity of the polypeptide is decreased in an animal subjected to pain, the therapeutic substance will increase the activity of the polypeptide relative to the activity of the same polypeptide in an animal subjected to the same pain, but not treated with the therapeutic agent.

The activity of the polypeptide molecules encoded by the polynucleotides indicated in Tables 1, 2, 3, 4, or 5 may be measured by any means known to those of skill in the art, and which are particular for the type of activity performed by the particular polypeptide. Examples of specific assays which may be used to measure the activity of particular polynucleotide products are shown below.

(a) G-protein coupled receptors

In one embodiment, the one or more of the differentially regulated polynucleotides of Tables 1, 2, 3, 4, or 5 may encode a G-protein coupled receptor. In one embodiment, the present invention provides a method of screening potential agonists and antagonists of the family of G-protein coupled receptors, including G_s, G_i, and G_q, encoded by the differentially expressed polynucleotides of the present invention by measuring changes in the activity of these receptors in the presence of a candidate agonist or antagonist.

1. G_i –coupled receptor screening

Cells (such as CHO cells, or primary cells) are stably transfected with the relevant receptor and with an inducible CRE-luciferase construct. Cells are grown in 50% Dulbecco's modified Eagle medium / 50% F12 (DMEM/F12) supplemented with 10% FBS, at 37°C in a

humidified atmosphere with 10% CO2 and are routinely split at a ratio of 1:10 every 2 or 3 days. Test cultures are seeded into 384 – well plates at an appropriate density (e.g. 2000 cells / well in 35 µl cell culture medium) in DMEM/F12 with FBS, and are grown for 48 hours (range: ~ 24 - 60 hours, depending on cell line). Growth medium is then exchanged against serum free medium (SFM; e.g. Ultra-CHO), containing 0,1% BSA. Test compounds dissolved in DMSO are diluted in SFM and transferred to the test cultures (maximal final concentration 10 µmolar), followed by addition of forskolin (~ 1 µmolar, final conc.) in SFM + 0,1% BSA 10 minutes later. In case of antagonist screening both, an appropriate concentration of agonist, and forskolin are added. The plates are incubated at 37°C in 10% CO2 for 3 hours. Then the supernatant is removed, cells are lysed with lysis reagent (25 mmolar phosphate-buffer, pH 7,8 , containing 2 mmolar DDT, 10% glycerol and 3% Triton X100). The luciferase reaction is started by addition of substrate-buffer (e.g. luciferase assay reagent, Promega) and luminescence is immediately determined (e.g. Berthold luminometer or Hamamatzu camera system).

2. G_s –coupled receptor screening

Cells (such as CHO, or primary cells) are stably transfected with the relevant receptor and with an inducible CRE-luciferase construct. Cells are grown in 50% Dulbecco's modified Eagle medium / 50% F12 (DMEM/F12) supplemented with 10% FBS, at 37°C in a humidified atmosphere with 10% CO2 and are routinely split at a ratio of 1:10 every 2 or 3 days. Test cultures are seeded into 384 – well plates at an appropriate density (e.g. 1000 or 2000 cells / well in 35 µl cell culture medium) in DMEM/F12 with FBS, and are grown for 48 hours (range: ~ 24 - 60 hours, depending on cell line). The assay is started by addition of test-compounds in serum free medium (SFM; e.g. Ultra-CHO) containing 0,1% BSA: Test compounds are dissolved in DMSO, diluted in SFM and transferred to the test cultures (maximal final concentration 10 µmolar, DMSO conc. < 0,6 %). In case of antagonist screening an appropriate concentration of agonist is added 5 – 10 minutes later. The plates are incubated at 37°C in 10% CO2 for 3 hours. Then the cells are lysed with 10 µl lysis reagent per well (25 mmolar phosphate-buffer, pH 7,8 , containing 2 mmolar DDT, 10% glycerol and 3% Triton X100) and the luciferase reaction is started by addition of 20 µl substrate-buffer per well (e.g. luciferase assay reagent, Promega). Measurement of luminescence is started immediately (e.g. Berthold luminometer or Hamamatzu camera system).

3. G_q –coupled receptor screening

Cells (such as CHO, or primary cells) are stably transfected with the relevant receptor. Cells expressing functional receptor protein are grown in 50% Dulbecco's modified Eagle medium / 50% F12 (DMEM/F12) supplemented with 10% FBS, at 37°C in a humidified atmosphere with 5% CO2 and are routinely split at a cell line dependent ratio every 3 or 4 days. Test cultures are seeded into 384 – well plates at an appropriate density (e.g. 2000 cells / well in 35 µl cell culture medium) in DMEM/F12 with FBS, and are grown for 48 hours (range: ~ 24 - 60 hours, depending on cell line). Growth medium is then exchanged against physiological salt solution (e.g. Tyrode solution). Test compounds dissolved in DMSO are diluted in Tyrode solution containing 0.1% BSA and transferred to the test cultures (maximal final concentration 10 µmolar). After addition of the receptor specific agonist the resulting Gq-mediated intracellular calcium increase is measured using appropriate read-out systems (e.g. calcium-sensitive dyes).

(b) Ion channels

Ion channels are integral membrane proteins involved in electrical signaling, transmembrane signal transduction, and electrolyte and solute transport. By forming macromolecular pores through the membrane lipid bilayer, ion channels account for the flow of specific ion species driven by the electrochemical potential gradient for the permeating ion. At the single molecule level, individual channels undergo conformational transitions ("gating") between the 'open' (ion conducting) and 'closed' (non conducting) state. Typical single channel openings last for a few milliseconds and result in elementary transmembrane currents in the range of 10-9 - 10-12 Ampere. Channel gating is controlled by various chemical and/or biophysical parameters, such as neurotransmitters and intracellular second messengers ('ligand-gated' channels) or membrane potential ('voltage-gated' channels). Ion channels are functionally characterized by their ion selectivity, gating properties, and regulation by hormones and pharmacological agents. Because of their central role in signaling and transport processes, ion channels present ideal targets for pharmacological therapeutics in various pathophysiological settings.

In one embodiment, the one or more of the differentially regulated polynucleotides of Tables 1, 2, 3, 4, or 5 may encode an ion channel. In one embodiment, the present invention provides a method of screening potential activators or inhibitors of channel activity encoded by the differentially expressed polynucleotides of the present invention. Screening for compounds interacting with ion channels to either inhibit or promote their activity can be based on (1.)

binding and (2.) functional assays in living cells (see for example, Hille, 1992, Ion Channels of Excitable Membranes Sunderland, MA, Sinauer Associates, Inc.; incorporated herein by reference in its entirety).

1. For ligand-gated channels, e.g. ionotropic neurotransmitter/hormone receptors, assays can be designed detecting binding to the target by competition between the compound and a labeled ligand.

2. Ion channel function can be tested functionally in living cells. Target proteins are either expressed endogenously in appropriate reporter cells or are introduced recombinantly. Channel activity can be monitored by (2.1) concentration changes of the permeating ion (most prominently Ca2+ ions), (2.2) by changes in the transmembrane electrical potential gradient, and (2.3) by measuring a cellular response (e.g. expression of a reporter gene, secretion of a neurotransmitter) triggered or modulated by the target activity.

2.1. Channel activity results in transmembrane ion fluxes. Thus activation of ionic channels can be monitored by the resulting changes in intracellular ion concentrations using luminescent or fluorescent indicators. Because of its wide dynamic range and availability of suitable indicators this applies particularly to changes in intracellular Ca2+ ion concentration ([Ca2+]i). [Ca2+]i can be measured, for example, by aequorin luminescence or fluorescence dye technology (e.g. using Fluo-3, Indo-1, Fura-2). Cellular assays can be designed where either the Ca2+ flux through the target channel itself is measured directly or where modulation of the target channel affects membrane potential and thereby the activity of co-expressed voltage-gated Ca2+ channels.

2.2. Ion channel currents result in changes of electrical membrane potential (Vm) which can be monitored directly using potentiometric fluorescent probes. These electrically charged indicators (e.g. the anionic oxonol dye DiBAC4(3)) redistribute between extra- and intracellular compartment in response to voltage changes. The equilibrium distribution is governed by the Nernst-equation. Thus changes in membrane potential results in concomitant changes in cellular fluorescence. Again, changes in Vm might be caused directly by the activity of the target ion channel or through amplification and/or prolongation of the signal by channels co-expressed in the same cell.

2.3. Target channel activity can cause cellular Ca2+ entry either directly or through activation of additional Ca2+ channel (see 2.1). The resulting intracellular Ca2+ signals

regulate a variety of cellular responses, e.g. secretion or gene transcription. Therefore modulation of the target channel can be detected by monitoring secretion of a known hormone/transmitter from the target-expressing cell or through expression of a reporter gene (e.g. luciferase) controlled by an Ca2+-responsive promoter element (e.g. cyclic AMP/ Ca2+-responsive elements; CRE).

(c) Transcription factors

In one embodiment, one or more of the differentially expressed polynucleotide sequences of Tables 1, 2, 3, 4, or 5 may encode a transcription factor. The activity of such a transcription factor may be measured, for example, by a promotor assay which measures the ability of the transcription factor to initiate transcription of a test sequence linked to a particular promotor. In one embodiment, the present invention provides a method for screening a test compound for its ability to modulate the activity of such a transcription factor by measuring the changes in the expression of a test gene which is regulated by a promoter which is responsive to the transcription factor.

A promoter assay can be set up with a human hepatocellular carcinoma cell HepG2 that is stably transfected with a luciferase gene under the control of a X (e.g. thyroid hormone) regulated promoter. The vector 2xIROluc, which can be used for transfection, carries a thyroid hormone responsive element (TRE) of two 12 bp inverted palindromes separated by an 8 bp spacer in front of a tk minimal promoter and the luciferase gene.

Test cultures are seeded in 96 well plates in serum - free Eagle's Minimal Essential Medium supplemented with glutamine, tricine, sodium pyruvate, non – essential amino acids, insulin, selen, transferrin, and are cultivated in a humidified atmosphere at 10 % CO2 at 37°C. After 48 hours of incubation serial dilutions of test compounds or reference compounds (L-T3, L-T4 e.g.) and costimulator if appropriate (final concentration 1 nM) are added to the cell cultures and incubation is continued for the optimal time (e.g. another 4-72 hours). The cells are then lysed by addition of buffer containing Triton X100 and luciferin and the luminescence of luciferase induced by T3 or other compounds is measured in a luminometer. For each concentration of a test compound replicates of 4 can be tested. EC50 – values for each test compound can be calculated by use of, for example, the Graph Pad Prism Scientific software.

Screening of Therapeutic agents that modulate the in vivo activity of proteins encoded by genes that are Differentially Expressed in Pain

The invention further provides for a screen of therapeutic compounds that modulate the in vivo activity of proteins encoded by genes that are differentially expressed in an animal subjected to pain (see Tables 1, 2, 3, 4, or 5). Methods for measuring changes in the in vivo activity of the proteins of the invention are well known in the art and include, but are not limited to, testing for changes in enzymatic activity, G coupled receptor activity or ion channel activity (as described herein under Polypeptide Activity); transcription factor function or the activity of signal tranduction pathway intermediates. Generally, these methods involve administering a candidate compound, as defined herein, or a placebo, to an animal that has been subjected to pain, preparing protein extracts from neural tissues and testing for a modulation in the protein activity in the extract in response to the candidate compound. In one embodiment, "protein activity" refers to the activity of a protein that is encoded by a gene that has been identified as a gene that is differentially expressed in an animal subjected to pain. In another embodiment, "protein activity" refers to the activity of one or more proteins whose activity is modulated by a protein that is encoded by a gene that has been identified as a gene that is differentially expressed in an animal subjected to pain.

In one embodiment, the "protein activity", according to the invention, refers to the ability of one or more ligands to bind to cell surface receptors that are differentially expressed in animals subjected to pain. For example, WO0102566A1 describes a screen for compounds that modulate the binding of glutamate to glutamate binding receptors.

In another embodiment, the "protein activity", according to the invention, is controlled by post-translational protein modification, e.g. phosphorylation or dephosphorylation. For example the protein, identified as being encoded by a gene that is differentially expressed in animals subjected to pain, may be a kinase, whose activity is modulated in response to a candidate compound either by direct phosphorylation or dephosphorylation. Alternatively, the activity of the kinase can be determined by assaying the phosphorylation of one or more substrates of the kinase. Methods for measuring the phosphorylation state of a protein are well known to a person skilled in the art. Typically radioactive phosphate is administered to a test animal that is then subjected to pain in the presence or absence of a therapeutic compound. Protein extracts are then prepared from neurological tissues and the protein of interest is isolated by immunoprecipitation and analyzed by SDS polyacrylamide electrophoresis. A 10% or more increase or decrease in the level of phosphorylation of the protein of interest in the presence of a compound relative to the

level of phosphorylation in the absence of the compound is indicative of a compound that modulates the "protein activity".

More generally, a gene, that is differentially expressed in animals subjected to pain, may encode a kinase or phosphatase that is part of a signal transduction pathway known in the art. If so, modulation of the activity of the kinase or phosphatase in response to a candidate compound can be determined by assaying the activity of pathway intermediates that are found downstream of the kinase or phosphatase in the pathway. For example, the activity of a kinase or phosphatase can be determined by measuring effects on gene expression or transcription factor activity. Methods for measuring differential gene expression or transcription factor function are well known in the art and are described supra. For example, the binding activity of a transcription factor to its cognate DNA binding site can be tested in protein extracts derived from treated animals using a mobility shift type analysis (see, e.g., Sambrook, Fritsch & Maniatis, 1989, Molecular Cloning: A Laboratory Manual, Second Edition; Short Protocols In Molecular Biology, (Ausubel et al., ed., 1995)). In addition, the ability of a transcription factor to activate transcription from a promoter containing one or more cognate DNA binding sites can also be tested using standard reporter type assays (GFP, CAT, lacZ) that are also well known in the art (See Ausubel et al; supra).

Modeling of Regulators

Computer modeling and searching technologies permit identification of compounds, or the improvement of already identified compounds, that can modulate the differentially expressed protein expression or activity. Having identified such a compound or composition, the active sites or regions are identified. Such sites might typically be the enzymatic active site, regulator binding sites, or ligand binding sites. The active site can be identified using methods known in the art including, for example, from the amino acid sequences of peptides, from the nucleotide sequences of nucleic acids, or from study of complexes of the relevant compound or composition with its natural ligand. In the latter case, chemical or X-ray crystallographic methods can be used to find the active site by finding where on the factor the complexed ligand is found.

Next, the three dimensional geometric structure of the active site is determined. This can be done by known methods, including X-ray crystallography, which can determine a complete molecular structure. On the other hand, solid or liquid phase NMR can be used to determine certain intramolecular distances. Any other experimental method of structure determination can

be used to obtain partial or complete geometric structures. The geometric structures may be measured with a complexed ligand, natural or artificial, which may increase the accuracy of the active site structure determined.

If an incomplete or insufficiently accurate structure is determined, the methods of computer based numerical modeling can be used to complete the structure or improve its accuracy. Any recognized modeling method may be used, including parameterized models specific to particular biopolymers such as proteins or nucleic acids, molecular dynamics models based on computing molecular motions, statistical mechanics models based on thermal ensembles, or combined models. For most types of models, standard molecular force fields, representing the forces between constituent atoms and groups, are necessary, and can be selected from force fields known in physical chemistry. The incomplete or less accurate experimental structures can serve as constraints on the complete and more accurate structures computed by these modeling methods.

Finally, having determined the structure of the active site, either experimentally, by modeling, or by a combination, candidate modulating compounds can be identified by searching databases containing compounds along with information on their molecular structure. Such a search seeks compounds having structures that match the determined active site structure and that interact with the groups defining the active site. Such a search can be manual, but is preferably computer assisted. These compounds found from this search are potential the differentially expressed protein modulating compounds.

Alternatively, these methods can be used to identify improved modulating compounds from an already known modulating compound or ligand. The composition of the known compound can be modified and the structural effects of modification can be determined using the experimental and computer modeling methods described above applied to the new composition. The altered structure is then compared to the active site structure of the compound to determine if an improved fit or interaction results. In this manner systematic variations in composition, such as by varying side groups, can be quickly evaluated to obtain modified modulating compounds or ligands of improved specificity or activity.

Analgesia Assays: In vivo testing of compounds/target validation for pain treatment

Acute Pain

Acute pain is measured on a hot plate mainly in rats. Two variants of hot plate testing are used: In the classical variant animals are put on a hot surface (52 to 56 °C) and the latency time is measured until the animals show nocifensive behavior, such as stepping or foot licking. The other variant is an increasing temperature hot plate where the experimental animals are put on a surface of neutral temperature. Subsequently this surface is slowly but constantly heated until the animals begin to lick a hind paw. The temperature which is reached when hind paw licking begins is a measure for pain threshold.

Compounds are tested against a vehicle treated control group. Substance application is performed at different time points via different application routes (intravenous (i.v.), intraperitoneal (i.p.), by mouth (p.o.), by inhalation (i.t.), Intracerebroventricular (i.c.v.), subcutaneous (s.c.), intradermal, or transdermal) prior to pain testing.

According to the invention, a candidate compound, may be administered to an animal which is subjected to an acute pain assay. Acute pain, measured according to the above assay, decreased by at least 10%, and preferably 20%, 40%, 60%, and up to 100% is then indicative of a candidate compound that decreases pain.

Persistent Pain

Persistent pain is measured with the formalin or capsaicin test, mainly in rats. A solution of 1 to 5% formalin or 10 to 100 µg capsaicin is injected into one hind paw of the experimental animal. After formalin or capsaicin application the animals show nocifensive reactions like flinching, licking and biting of the affected paw. The number of nocifensive reactions within a time frame of up to 90 minutes is a measure for intensity of pain.

Compounds are tested against a vehicle treated control group. Substance application is performed at different time points via different application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to formalin or capsaicin administration.

According to the invention, a candidate compound, may be administered to an animal which is subjected to an persistent pain assay. Persistent pain, measured according to the above assay, decreased by at least 10% and preferably 20%, 40%, 60%, and up to 100% is then indicative of a candidate compound that decreases pain.

Neuropathic Pain

Neuropathic pain is induced by different variants of unilateral sciatic nerve injury mainly in rats. The operation is performed under anesthesia. The first variant of sciatic nerve injury is produced by placing loosely constrictive ligatures around the common sciatic nerve (Bennett and Xie, Pain 33 (1988): 87-107). The second variant is the tight ligation of about the half of the diameter of the common sciatic nerve (Seltzer et al., Pain 43 (1990): 205-218). In the next variant, a group of models is used in which tight ligations or transections are made of either the L5 and L6 spinal nerves, or the L5 spinal nerve only (Kim SH; Chung Jm, An experimental-model for peripheral neuropathy produced by segmental spinal nerve ligation in the rat, Pain 50 (3) (1992): 355-363). The fourth variant involves an axotomy of two of the three terminal branches of the sciatic nerve (tibial and common peroneal nerves) leaving the remaining sural nerve intact whereas the last variant comprises the axotomy of only the tibial branch leaving the sural and common nerves uninjured. Control animals are treated with a sham operation.

Postoperatively, the nerve injured animals develop a chronic mechanical allodynia, cold allodynioa, as well as a thermal hyperalgesia. Mechanical allodynia is measured by means of a pressure transducer (electronic von Frey Anesthesiometer, IITC Inc.-Life Science Instruments, Woodland Hills, SA, USA; Electronic von Frey System, Somedic Sales AB, Hörby, Sweden). Thermal hyperalgesia is measured by means of a radiant heat source (Plantar Test, Ugo Basile, Comerio, Italy), or by means of a cold plate of 5 to 10 °C where the nocifensive reactions of the affected hind paw are counted as a measure of pain intensity. A further test for cold induced pain is the counting of nocifensive reactions, or duration of nocifensive responses after plantar administration of acetone to the affected hind limb. Chronic pain in general is assessed by registering the circadanian rhytms in activity (Surjo and Arndt, Universität zu Köln, Cologne, Germany), and by scoring differences in gait (foot print patterns; FOOTPRINTS program, Klapdor et al., 1997. A low cost method to analyse footprint patterns. J. Neurosci. Methods 75, 49-54).

Compounds are tested against sham operated and vehicle treated control groups. Substance application is performed at different time points via different application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to pain testing.

According to the invention, a candidate compound, may be administered to an animal, which is subjected to an neuropathic pain assay. Neuropathic pain, measured according to the above assay, decreased by at least 10% and preferably 20%, 40%, 60%, and up to 100% is then indicative of a candidate compound that decreases pain.

Inflammatory Pain

Inflammatory pain is induced mainly in rats by injection of 0.75 mg carrageenan or complete Freund's adjuvant into one hind paw. The animals develop an edema with mechanical allodynia as well as thermal hyperalgesia. Mechanical allodynia is measured by means of a pressure transducer (electronic von Frey Anesthesiometer, IITC Inc.-Life Science Instruments, Woodland Hills, SA, USA). Thermal hyperalgesia is measured by means of a radiant heat source (Plantar Test, Ugo Basile, Comerio, Italy, Paw thermal stimulator, G. Ozaki, University of California, USA). For edema measurement two methods are being used. In the first method, the animals are sacrificed and the affected hindpaws sectioned and weighed. The second method comprises differences in paw volume by measuring water displacement in a plethysmometer (Ugo Basile, Comerio, Italy).

Compounds are tested against uninflamed as well as vehicle treated control groups. Substance application is performed at different time points via different application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to pain testing.

According to the invention, a candidate compound, may be administered to an animal which is subjected to an inflammatory pain assay. Inflammatory pain, measured according to the above assay, decreased by at least 10% and preferably 20%, 40%, 60%, and up to 100% is then indicative of a candidate compound that decreases pain.

Diabetic Neuropathic Pain

Rats treated with a single intraperitoneal injection of 50 to 80 mg/kg streptozotocin develop a profound hyperglycemia and mechanical allodynia within 1 to 3 weeks. Mechanical allodynia is measured by means of a pressure transducer (electronic von Frey Anesthesiometer, IITC Inc.-Life Science Instruments, Woodland Hills, SA, USA).

Compounds are tested against diabetic and non-diabetic vehicle treated control groups. Substance application is performed at different time points via different application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to pain testing.

According to the invention, a candidate compound, may be administered to an animal which is subjected to an Diabetic Neuropathic pain assay. Diabetic Neuropathic pain, measured according to the above assay, decreased by at least 10% and preferably 20%, 40%, 60%, and up to 100% is then indicative of a candidate compound that decreases pain.

In one embodiment, the candidated compounds which are administered to an animal subjected to one or more of the above pain stimuli, can be a candidate compound which has been previously determined to regulate the expression of one or more of the differentially expressed polynucleotide sequences indicated in Tables 1, 2, 3, 4, or 5, and/or previously determined to regulate the activity of a protein encoded by one or more of the differentially expressed polynucleotides indicated in Table 1, 2, 3, 4, or 5.

Dosage and Administration

Therapeutic agents of the invention are administered to an animal, preferably in a biologically compatible solution or a pharmaceutically acceptable delivery vehicle, by ingestion, injection, inhalation or any number of other methods. For embodiments where the therapeutic agent is a vector comprising an antisense sequence, a sequence encoding a ribozyme, or a sequence designed to supplement a down regulated sequence in an animal subjected to pain, the vectors may be administered as a pharmaceutical formulation, or may be administered using any method known in the art including microinjection, transfection, transduction, and *ex vivo* delivery. The dosages administered will vary from patient to patient; a "therapeutically effective dose" is determined, for example but not limited to, by the level of enhancement of function (*e.g.*, for a nucleic acid sequence which is overexpressed by at least 1.4 fold in an animal subjected to pain relative to a naïve animal, a therapeutically effective dose is one which reduces the level of overexpression of the sequence to less than 1.4 fold. The converse would define a therapeutically effective dose for increasing the expression of an under-expressed sequence).

A therapeutic agent according to the invention is preferably administered in a single dose. This dosage may be repeated daily, weekly, monthly, yearly, or until the nucleic acid sequence is no longer differentially expressed.

Pharmaceutical Compositions

The invention provides for compositions comprising a therapeutic agent according to the invention admixed with a physiologically compatible carrier. As used herein, "physiologically compatible carrier" refers to a physiologically acceptable diluent such as water, phosphate buffered saline, or saline, and further may include an adjuvant. Adjuvants such as incomplete Freund's adjuvant, aluminum phosphate, aluminum hydroxide, or alum are materials well known in the art.

The invention also provides for pharmaceutical compositions. In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically acceptable carrier preparations which is used pharmaceutically.

Pharmaceutical compositions for oral administration are formulated using pharmaceutically acceptable carriers well known in the art in dosages suitable for oral administration. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for ingestion by the patient.

Pharmaceutical preparations for oral use are obtained through a combination of active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are carbohydrate or protein fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose such as methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxymethyl cellulose; and gums including arabic and tragacanth; and proteins such as gelatin and collagen. If desired, disintegrating or solubilizing agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, alginic acid, or a salt thereof, such as sodium alginate.

Dragee cores are provided with suitable coatings such as concentrated sugar solutions, which may also contain gum arabic, talc, polyvinylpyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound, i.e., dosage.

Pharmaceutical preparations which are used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating such as glycerol or sorbitol. Push-fit capsules can contain active ingredients mixed with a filler or binders such as lactose or starches, lubricants such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycol with or without stabilizers.

Pharmaceutical formulations for parenteral administration include aqueous solutions of active compounds. For injection, the pharmaceutical compositions of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hank's

solution, Ringer' solution, or physiologically buffered saline. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Additionally, suspensions of the active solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

For nasal administration, penetrants appropriate to the particular barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

The pharmaceutical compositions of the present invention may be manufactured in a manner known in the art, e.g. by means of conventional mixing, dissolving, granulating, dragee-making, levitating, emulsifying, encapsulating, entrapping or lyophilizing processes.

The pharmaceutical composition may be provided as a salt and are formed with many acids, including but not limited to hydrochloric, sulfuric, acetic, lactic, tartaric, malic, succinic, etc... Salts tend to be more soluble in aqueous or other protonic solvents that are the corresponding free base forms. In other cases, the preferred preparation may be a lyophilized powder in 1mM-50 mM histidine, 0.1%-2% sucrose, 2%-7% mannitol at a pH range of 4.5 to 5.5 that is combined with buffer prior to use.

After pharmaceutical compositions comprising a therapeutic agent of the invention formulated in a acceptable carrier have been prepared, they are placed in an appropriate container and labeled for treatment of an indicated condition with information including amount, frequency and method of administration.

EXAMPLES

The examples below are non-limiting and are merely representative of various aspects and features of the present invention.

Example 1. Identification of differentially expressed nucleic acid sequences

The present invention relates to a method for the identification of nucleic acid sequences and/or genes which are differentially expressed in an animal which has been subjected to pain. In one embodiment, the animal is a pain model, that is, the animal has been artificially

985

manipulated such that it meets the criteria for a state of pain as described above. In one embodiment the animal pain model is produced by transection of the sciatic nerve (axotomy). In an alternate embodiment, the animal pain model is the spared nerve injury model (SNI; Decosterd and Woolf, 2000 *Pain* 87: 149) in which one of the terminal branches of the sciatic nerve is spared from axotomy. In a further alternate embodiment, the animal pain model is an inflammation model (Stein et al., (1988) *Pharmacol Biochem Behav* 31: 445-451; Woolf et al., (1994) *Neurosci.* 62, 327-331) in which an irritant such as CFA is injected into an animal to induce inflammation.

Animal pain models

Axotomy of the sciatic nerve was performed on adult (200-250 g) male Sprague-Dawley rats. Under halothane (2%) anesthesia, the skin on the lateral surface of the thigh was incised and an incision made directly through the biceps femoris muscle exposing the sciatic nerve. The axotomy procedure involves transecting the sciatic nerve following ligation. The sciatic nerve was tight-ligated with 5.0 silk and sectioned distal to the ligation, removing 2-4 mm of the distal nerve stump. Great care was taken to avoid any contact with or transection of any collateral branches of the sciatic nerve proximal to the transection site, or any cutaneous nerve branches. Muscle and skin were closed in two layers, and animals were allowed to recover for 3-5 days prior to testing for signs of pain including mechanical allodynia, mechanical hyperalgesia, cold allodynia, and heat hyperalgesia using the criteria described above. Sham control animals (naïve) involved exposure of the sciatic nerve and its branched without any lesion.

The SNI nerve injury model was performed on adult (200-250 g) male Sprague-Dawley rats. Under halothane (2%) anesthesia, the skin on the lateral surface of the thigh was incised and a section made directly through the biceps femoris muscle exposing the sciatic nerve and its three terminal branches: the sural, common peroneal and tibial nerves.

The SNI procedure comprises an axotomy and ligation of the tibial and common peronial nerves leaving the sural nerve intact. The common peroneal and the tibial nerves were tight-ligated with 5.0 silk and sectioned distal to the ligation, removing 2-4 mm of the distal nerve stump. Great care was taken to avoid any contact with or stretchnig of the intact sural nerve. Muscle and skin were closed in two layers and animals were allowed to recover for at least one week prior to testing for signs of pain including mechanical allodynia, mechanical hyperalgesia,

cold allodynia, and heat hyperalgesia using the criteria described above. Sham control animals (naïve) involved exposure of the sciatic nerve and its branched without any lesion.

The inflammation animal pain model was performed on adult male Sprague-Dawley rats (10-11 weeks old, 300-350 g). Inflammation was induced by an intra-plantar injection of complete Freund's adjuvant (CFA, Sigma,1 µl – 1 ml) into the left hind paw of rats under halothane (2.5%) anesthesia, producing an area of erythema, edema and tenderness restricted to the hindpaw (Stein et al., (1988) *Pharmacol Biochem Behav* 31: 445-451; Woolf et al., (1994) *Neurosci.* 62, 327-331). Animals were subsequently tested for signs of pain including mechanical allodynia, mechanical hyperalgesia, cold allodynia, and heat hyperalgesia using the criteria described above.

Total RNA isolation

Following the surgical procedures described above and testing to insure that the axotomy and SNI model animals met the pain criteria described, control and pain model animals were rapidly killed by decapitation. Axotomy model animals were killed 3 days following axotomy, and SNI model animals were killed 10-15 days following surgery.

The dorsal root ganglia (DRG) from spinal levels L4-L5 were removed from the SNI, axotomy, and control animals and snap-frozen in a dry ice/ethanol slurry. DRGs from the two spinal levels were pooled for each animal and total RNA was extracted using Trizol (Invitrogen) according to the manufacturers instructions. Briefly, tissue samples were homogenized in a ground glass homogenizer in 1 ml of Trizol reagent per 50-100 mg of tissue. The samples were incubated for 5 min. at 15-30° C to permit the complete dissociation of nucleoprotein complexes. Subsequently, 0.2 ml of chloroform was added per 1 ml of Trizol reagent. Samples were agitated and incubated at 15-30° C for 2 to 3 minutes. Samples were then centrifuged at no more than 12,000 x g for 15 minutes at 2-8° C. The aqueous phase was then transferred to a fresh tube and the RNA was precipitated by mixing with 0.5 ml of isopropyl alcohol per 1 ml Trizol reagent used for the initial homogenization. Samples were incubated at 15-30° C for 10 minutes and centrifuged at 12,000 x g for 10 minutes. The supernatant is then removed, and the RNA pellet was washed with 75% ethanol. The RNA pellet is then air dries and resuspended in either RNase-free water or 0.5% SDS solution. The integrity of the RNA samples was verified on a 1% agarose gel, and the RNA was quantified by measuring absorbance at 260/280 mm. cRNA was then prepared from 10 µg of total RNA using techniques that are well known in the art.

Briefly, total RNA (7 to 10 µg) was isolated and reverse transcribed using a primer consisting of oligo-dT coupled to a T7 RNA polymerase binding site. The cDNA was made double stranded and biotinylated cRNA was synthesized using T7 polymerase. Unincorporated nucleotides were removed, and the cRNA was quantitated using methods known to those of skill in the art; a yield of cRNA between 25 and 80 µg was typical.

Array hybridization

The cRNA samples from axotomy, SNI and naïve animals were randomly sheared to an approximate length of 50 nucleotides and subsequently hybridized to an Affymetrix rat genome U34 gene chip set. Briefly, labeled nucleic acid is denatured by heating for 2 minutes at 100° C, and incubated at 37° C of 20-30 minutes before being placed on a nucleic acid array under a 22 mm x 22 mm glass cover slip. Hybridization is carried out at 65° C for 14 to 18 hours in a custom slide chamber with humidity maintained by a small reservoir of 3 x SSC. The array is washed by submersion and agitation for 2-5 min in 2X SSC with 0.1% SDS, followed by 1X SSC, and 0.1X SSC. Finally, the array is dried by centrifugation for 2 minutes in a slide rack in a Beckman GS-6 tabletop centrifuge in Microplus carriers at 650 RPM for 2 min.

External standards were included in each hybridization to control for hybridization efficiency, to test for sensitivity and assist in the comparisons between data sets from different experiments. These external standards are cRNA transcribed from the bacterial genes *bio b, bio c, bio d, cre, thr, and phe.* The first hybridization was against a Test Chip, which contains probes against human, mouse and yeast mRNAs as well as probes against the exogenously added control RNA. The Test Chips are designed to determine the quality of the cRNA mixture. Stringent washing in the fluidics station reduces non-specific hybridization and the hybridized biotinylated cRNA was detected by incubation with phycoerythrin-streptavidin and was quantitated by scanning using the Hewlett-Packard GeneArray laser scanner. Following positive analysis of the Test Chip, the same hybridization mixture was then added to the Rat Genome U34 gene chip set which monitors the expression of >24,000 genes and EST clusters. The sequences include all rat sequence clusters from Build #34 of the UniGene Datablse (created from GenBank 107/dbEST 11/18/98) and supplemented with additional annoteted gene sequences from GenBank 110. The chips were hybridized, reacted with phycoerythrin-streptavidin, washed and then incubated with a polyclonal anti-streptavidin antibody coupled to phycoerythrin as an amplification step to aid in the detection of lower abundance transcripts.

Following further washing, the expression chip was scanned as above. Analysis of the scanned data was performed using GeneChip software.

Gene selection

Known or EST gene sequences were first selected as being potentially differentially expressed based on the fold change in hybridization between the naïve animals and either the axotomy or SNI pain models. This was measured as the ratio of the expression level, measured as the intensity of the hybridization signal of the cRNA probe on the microarray for a specific gene, of either SNI or axotomy to naïve. Based on previous studies which demonstrate that the expression of the heat shock protein Hsp27 in increased 1.5 fold after axotomy, a 1.4 fold change in expression in either the axotomy or SNI models relative to naïve was chosen as a numerical cutoff for differential expression. Genes identified as being differentially expressed based on the measurement of an at least 1.4 fold change in expression are shown in tables 1, 2, 3, 4, or 5. Table 1 shows a group of genes which have been previously suggested to exhibit regulated expression in pain models, but which have been evaluated for purposes of the present invention as being differentially expressed by at least 1.4 fold in both a rat axotomy pain model and a SNI pain model relative to the expression level in an animal not subjected to pain. Thus, from the genes and polynucleotides shown in Table 1, only those showing a axotomy/naïve or SNI/naïve ratio of +/- 1.4 or greater were identified as being differentially expressed. Tables 2-3 show a number of genes which were identified by the methods of the present invention as being differentially expressed by at least 1.4 fold in an animal subjected to a nerve injury or inflammatory pain model. In addition, the polynucleotides indicated in Table 2, have been firther confirmed as beind differentially expressed based on triplicate expression analysis (i.e., samples from three different animals hybridized to three different microarrays, wherein samples are obtained from several different animal pain models, and wherein the polynucleotide sequences are differentially expressed by at least 1.2 fold, with a significance of $p<0.05$ in at least one pain model). Table 4 shows a group of genes which exhibit an at least 1.4 fold increase in expression in the inflammation pain model. Table 5 shows a group of genes which exhibit an at least 1.4 fold decrease in expression in the inflammation pain model. The data in Tables 1, 3, 4, and 5 represent the average hybridization measurements obtained from at least two rat gene chips.

Genes identified as being differentially expressed based on an at least 1.4 fold change in expression were then screened by Northern analysis to verify differential expression.

Northern analysis

For each gene suggested to be differentially expressed based on the microarray data, RT-PCR was performed on DRG total RNA obtained from the axotomy, SNI and naïve animal groups as described above. RT-PCR was performed according to techniques known in the art. The cDNA fragments generated in this manner were subsequently cloned into a PCRII vector using the TA cloning kit (Invitrogen). The identity of each fragment was verified by sequencing in each direction from the T3 and T7 polymerase sites present in the cloning vector. The cDNA molecules produced in this manner were then used to produce ^{32}P-labeled cDNA probes using the Prime-It kit from Stratagene. Subsequently, 5 to 10 μg of total RNA isolated from axotomy, SNI and naïve DRGs were separated on an agarose/formaldehyde gel in 1X MOPS buffer. Following staining with ethidium bromide and visualization under ultra violet light to determine the integrity of the RNA, the RNA is hydrolyzed by treatment with 0.05M NaOH/1.5MNaCl followed by incubation with 0.5M Tris-Cl (pH 7.4)/1.5M NaCl. The RNA is transferred to a commercially available nylon or nitrocellulose membrane (e.g. Hybond-N membrane, Amersham, Arlington Heights, IL) by methods well known in the art (Ausubel et al., supra, Sambrook et al., supra). Following transfer and UV cross linking, the membrane is hybridized with a ^{32}P-labeled cDNA probe, having a sequence complementary to the mRNA sequences identified as being differentially expressed by microarray analysis, in hybridization solution (e.g. in 50% formamide/2.5% Denhardt's/100-200mg denatured salmon sperm DNA/0.1% SDS/5X SSPE) overnight at 65°C. The hybridization conditions can be varied as necessary as described in Ausubel et al., supra and Sambrook et al., supra. Following hybridization, the membrane is washed at room temperature in 2X SSC/0.1% SDS, at 42°C in 1X SSC/0.1% SDS, at 65°C in 0.2X SSC/0.1% SDS, and exposed to film overnight with an intensifying screen at -80° C. The stringency of the wash buffers can also be varied depending on the amount of background signal (Ausubel et al., supra). The film was subsequently developed and the intensity bands corresponding to the radiolabeled probe hybridized to RNA were quantified using methods known to those of skill in the art, for example, by digitizing the film and analyzing the band intensity with a computer software program such as NIH Image (NIH, Bethesda, MD).

Figure 1 shows an example of Northern data which confirms the differential expression, or lack thereof, of 22 genes which were initially screened by microarray analysis of cRNA samples obtained from animals subjected to the axotomy pain model. Table 8 shows the

correlation of the data obtained from the microarray analysis for these 22 genes and the data obtained by Northern analysis.

Example 2. Verification by *In situ* Hybridization

In addition to verification of differential expression using Northern analysis, the present invention provides that the differential expression of genes in an animal subjected to pain may be confirmed using in situ hybridization.

In situ hybridization is carried out on fresh frozen, 5μm thick sections of the dorsal root ganglia from spinal levels L4-L5 obtained from animals subjected to pain, using isotopically-labeled probes. Forty-eight base pair oligonucleotide probes are designed to have 50% G-C content and be complementary to and selective for the desired mRNA. Probes are 3'-end labeled with ^{35}S or ^{33}P-dATP using a terminal transferase reaction and purified through a spin column. Hybridization is carried out such that homologies greater than 90% are required for detection of transcripts (Dagerlind et al., '92 *Histochemistry* 98:39). Generally, slides are brought to room-temperature and covered with a hybridization solution (50% formamide, 1x Dendhardt's solution, 1% sarcosyl, 10% dextran sulphate, 0.02M phosphate buffer, 4x SSC, 200 nM DTT, 500 mg/ml salmon sperm DNA) containing 107 cmp/ml of labeled probe. Slides are incubated in a humidified chamber at 43°C for 14-18 hours, then washed 4 x 15min in 1x SSC at 55oC. In the final rinse, slides are brought to room temperature, washed in dH2O, dehydrated in ethanol and air dried.

Autoradiograms are generated by dipping slides in NTB2 nuclear track emulsion and storing the dark at 4°C. Prior to conventional developing and fixation, sections are allowed to expose for 1-12 weeks, depending on the abundance of transcript. Unstained tissue is viewed under darkfield conditions using a fiber-optic darkfield stage adapter (MVI), while stained tissue is examined under brightfield conditions. Control experiments are conducted to confirm the specificity of the oligonucleotide probes. Sections are hybridized with labeled probe, labeled probe with a 1,000-fold excess of cold probe, or labeled probe with a 1,000-fold excess of another, dissimilar cold probe of the same length and similar G-C content.

The use of serial, thin sections permits the identification of the same cells in adjacent sections, allowing for comparisons to be made with other markers by in situ hybridization or immunohistochemistry. The technique unlike non-isotopic in situ using digoxygenin labeled riboprobes is suited to screening more than detailed anlysis of co-expression of multiple markers.

Figures 2 and 3 show the results of *in situ* hybridization verification of the differential expression of five genes (GTPcyclo, IES-JE, CCHL2A, VGF, SNAP, c-jun, and TrkA) in the dorsal root ganglia of a rat axotomy pain model and a rat spared nerve injury pain model.

Example 3. Verification of differential expression by Real-time PCR

In addition to verification of differential expression by Northern analysis or *in situ* hybridization, the differential expression of genes in an animal subjected to pain may be verified using real-time PCR and TaqMan® probes. The technique of real-time PCR is well known in the art (see, for example, U.S. Pat. Nos. 5,691,146; 5,779,977; 5,866,336; and 5,914,230).

cDNA samples obtained from a rat axotomy pain model were amplified using primers specific for 19 genes which had previously been examined by microarray analysis and SYBR Green I as the double stranded DNA binding dye. PCR products were generated using an ABI 7700 sequence detection system (Applied Biosystems, Foster City, CA). A comparison of the expression level measured by microarray analysis and that obtained by real-time PCR is shown in Table 9. A close correlation can be seen between the differential expression, or lack thereof, of genes examined by microarray analysis and using the Taqman® technique.

Example 4. Triplicate Analysis

As described above, a polynucleotide sequence is identified as being differentially regulated in an animal subjected to pain relative to an animal not subjected to the same pain if the sequence is differentially expressed by at least 1.4 fold, and additionally, if the differential expression attains a statistical significance over at least three replicate screens, in at least on pain model, with a p-value of less than 0.05. This example describes how to perform such a statistical analysis, using the axotomy and SNI pain models.

Surgical procedures.

Adult male Sprague Dawley rats (200-300g) are anesthetized with halothane. For the sciatic nerve transection (axotomy), the left sciatic nerve is exposed at the mid thigh level, ligated with 3/0 silk and sectioned distally. The wound is sutured in two layers, and the animals were allowed to recover.

Tissue and RNA preparation.

Animals are terminally anesthetized with CO_2, the L4 and L5 DRGs rapidly removed, and stored at -80°C. Total RNA is extracted from homogenized DRG samples using acid phenol extraction (TRIzol reagent, Gibco-BRL). RNA concentration is evaluated by A_{260} measurement and quality assessed by electrophoresis on a 1.5% agarose gel. Each RNA sample used for hybridization of each array can be extracted, for example, from rat L4 and L5 DRGs (10 ganglia pooled from 5 animals, per sample).

Microarray Analysis

Affymetrix rat genome U34A oligonucleotide microarrays, representing 8799 known transcripts and expressed sequence tags (ESTs), can be used (Affymetrix, Santa Clara, CA). Oligonucleotides are arranged in pairs corresponding to different regions of the target mRNA with multiple probe pairs. Each probe pair consists of a 25 nucleotide perfect match (PM) to the target region coupled with a 25-mer with a single mismatch (MM) at the 13th nucleotide. Transcript abundance is estimated by analysis of signal intensity of the PM/MM pairs. The arrays are hybridized with biotin-labeled cRNA, prepared as per standard Affymetrix protocol. Briefly, total RNA (8 μg) from DRGs was reverse transcribed using an oligo-dT primer coupled to a T7 RNA polymerase binding site. Double-stranded cDNA can be made and biotinylated-cRNA synthesized using T7 polymerase. The cRNA is then hybridized for about 16 hours to an array, followed by binding with a streptavidin-conjugated fluorescent marker, and then incubated with a polyclonal anti-streptavidin antibody coupled to phycoerythrin as an amplification step. Following washing, the chips are scanned with a Hewlett-Packard GeneArray laser scanner and data analyzed using GeneChip software. External standards can be included to control for hybridization efficiency and sensitivity.

Hybridization levels for each species of mRNA detected on the arrays are expressed by intensity (signal) and as present (P), marginal (M) or absent (A) calls, calculated by Affymetrix software (MAS 5.0, $\alpha 1 = 0.04$ $\alpha 2 = 0.06$). For calculation of signal values, each array is scaled to a target signal of 2500 across all probe sets, to allow comparison between arrays.

The arrays are grouped for two comparisons: two triplicate sets of naïve data compared with one another, and one triplicate naïve set compared with one triplicate post-axotomy set. The individual naïve arrays included in each triplicate set are picked randomly. A probe set is determined undetected if it received an A call in all of the six arrays involved in the comparison. Detected are Present or Marginal by MAS5.0 in at least one array for each analysis. Mean signal

and standard deviations are calculated for each detected probe set. The p-value for rejecting the null hypothesis that the mean signals were equal between the two triplicate sets is calculated using an unpaired, two-tailed t-test for independent samples with unequal variance (Satterthwaite's method). Fold-differences between the mean signals (A and B) in the two triplicate sets is calculated as max(A, B) / min(A, B) with down regulation relative to naïve expressed as negative.

As noted above, a polynucleotide sequence is considered to be differentially expressed according to the present invention if it is differentially expressed by at least 1.4 fold in an animal subjected to pain relative to an animal not subjected to the same pain, and optionally, is also statistically significantly differentially expressed with a p-value of less than 0.05 across at least three replicate expression screens.

Example 5. Pain-specific Microarray Construction

A microarray according to the invention was constructed as follows.

cDNA samples obtained from the dorsal root ganglia of either naïve animals or animals which have been subjected to pain are amplified using primers specific for the genes which have been identified as being differentially expressed using the methods described above. PCR products (~40 ul) in the same 96-well tubes used for amplification, are precipitated with 4 ul (1/10 volume) of 3M sodium acetate (pH 5.2) and 100 ul (2.5 volumes) of ethanol and stored overnight at –20°C. They are then centrifuged at 3,300 rpm at 4°C for 1 hour. The obtained pellets were washed with 50 ul ice-cold 70% ethanol and centrifuged again for 30 minutes. The pellets are then air-dried and resuspended well in 20ul 3X SSC overnight. The samples are then deposited either singly or in duplicate onto polylysine-coated slides (Sigma Cat. No. P0425) using a robotic GMS 417 arrayer (Genetic MicroSystems, MA). The boundaries of the DNA spots on the microarray are marked with a diamond scriber. The invention provides for arrays wherein 10-20,000 PCR products are spotted onto a solid support to prepare an array.

The arrays are rehydrated by suspending the slides over a dish of warm particle free ddH_20 for approximately one minute (the spots will swell slightly but not run into each other) and snap-dried on a 70-80°C inverted heating block for 3 seconds. DNA is then UV crosslinked to the slide (Stratagene, Stratalinker, 65 mJ – set display to "650" which is 650 x 100 uJ). The arrays are placed in a slide rack. An empty slide chamber is prepared and filled with the

methyl-2-pyrrolidinone (rapid addition of reagent is crucial); immediately after the last flake of succinic anhydride dissolved, 21.0 ml of 0.2 M sodium borate is mixed in and the solution is poured into the slide chamber. The slide rack is plunged rapidly and evenly in the slide chamber and vigorously shaken up and down for a few seconds, making sure the slides never leave the solution, and then mixed on an orbital shaker for 15-20 minutes. The slide rack is then gently plunged in 95°C dd$H_2$0 for 2 minutes, followed by plunging five times in 95% ethanol. The slides are then air dried by allowing excess ethanol to drip onto paper towels. The arrays are then stored in the slide box at room temperature until use.

Example 6. Therapeutic Agent Screening

A candidate agent that increases or decreases the expression of a polynucleotide sequence that is differentially expressed in the sensory neurons of an animal subjected to pain is screened according to the following method.

An animal that has been subjected to pain is treated with a candidate agent for varying amounts of time. Typically an animal is treated by systemic administration of a candidate agent, such as by intravenous administration, on a hourly, daily, or weekly dosing schedule. Following administration, the animals are killed, and the dorsal root gangila are removed and used to prepare cRNA samples as described above. The cRNA samples are then hybridized to a pain-specific microarray, constructed according to the method described above. The hybridization of the cRNA samples to the microarray can be used to determine the level of expression of the genes in the animal subjected to pain which correspond to the differentially expressed genes comprising the microarray. Thus any changes in the predicted differential expression of a gene in an animal treated with a candidate agent is indicative of that agent being capable of increasing or decreasing the expression of a gene which is known to be differentially expressed in an animal subjected to pain.

Example 7: In vivo protein activity screening

Microarrays can be used to screen *in vivo* for genes that are regulated in pain as a result of the activity of specific protein signaling molecules. To do this, the changes in gene expression produced in the pain models are compared with the changes in gene expression produced in the same models when a particular signaling molecule is neutralized or inhibited by preventing its synthesis, release, transport, binding to a receptor or activation of a cellular response. Any

resultant difference in gene expression profile will represent the contribution of the signaling molecule. Further confirmation can be produced by the administration of the signaling molecule *in vivo* to see if it induces a change in gene regulation.

Such an analysis has been performed looking at the contribution of the neurotrophin nerve growth factor (NGF) to inflammatory pain. Inflammation is known to produce an increase in NGF at the site of the inflammation and this acts on its high affinity receptor TrkA expressed on sensory neurons to change transcription of NGF-regulated genes in the sensory neuron cell body in the DRG. The pattern of expression of genes after inflammation induced in vivo by intraplantar CFA (at 3, 12 24 hrs and 5 days) was compared with naïve non-inflamed animals to detect inflammation-induced genes. This gene expression profile was then compared with arrays produced from RNA from inflamed animals treated with a neutralizing anti-NGF antibody. One example of a gene that was upregulated by CFA, but whose level did not increase in CFA animals treated with antiNGF was the NF-kappaB inhibitor alpha (I kappa B). I kappa B alpha was also upregulated 12 and 24 hrs after intraplantar NGF injection showing that it is an NGF regulated inflammatory-induced gene.

Affymetrix accession #X63594cds_g_at X63594cds RRRLIF1 R.rattus RL/IF-1 mRNA

	CFA	NGF	CFA + anti-NGF
	Fold	Fold	Fold
Ni			
3h	-1		
6h	8.5		
12h	2.1	3.5	-1.8
24h	3.4	1.5	1.4
2d	1.1		
5d	1.6		

Affymetrix accession numbers #X63594cds_g_at and X63594cds RRRLIF1 refer to sequences depicted in Table 2.

OTHER EMBODIMENTS

Other embodiments will be evident to those of skill in the art. It should be understood that the foregoing detailed description is provided for clarity only and is merely exemplary. The spirit and scope of the present invention are not limited to the above examples, but are encompassed by the following claims.

CLAIMS

1. A composition comprising two or more isolated polynucleotides, wherein each of said two or more isolated polynucleotides is selected from the group consisting of:

(a) a polynucleotide comprising any of the polynucleotides specified in Table 1-2 in the columns designated "rat gene" and "human gene", and wherein at least one of said two or more isolated polynucleotides is unique toTable 2 in the columns designated "rat gene" and "human gene";

(b) a polynucleotide encoding an amino acid sequence selected from the group consisting of:

(i) amino acid sequences which are homologue to any of the amino acid specified in Table 2 in the columns designated "rat protein" and "human protein" by at least the homology as specified for the respective sequence in Table 2 in the column designated "%homology" and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(ii) the amino acid specified in Table 2 in the columns designated "rat protein" and "human protein";

(c) a polynucleotide which hybridizes under high stringency conditions to a polynucleotide specified in (a) to (b) and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(d) a polynucleotide the nucleic acid sequence or which deviates from the nucleic acid sequences specified in (a) to (c) due to the degeneration of the genetic code and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(e) a polynucleotide which represents a fragment, derivative or allelic variation of a nucleic acid sequence specified in (a) to (d) and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier".

2. A plurality of vectors each comprising an isolated polynucleotide, wherein each of said two or more isolated polynucleotides is selected from the group consisting of:

(a) a polynucleotide comprising any of the polynucleotides specified in Table 1-2 in the columns designated "rat gene" and "human gene", and wherein at least one of said two or more isolated polynucleotides is unique to Table 2 in the columns designated "rat gene" and "human gene";

(b) a polynucleotide encoding an amino acid sequence selected from the group consisting of:

(i) amino acid sequences which are homologue to any of the amino acid specified in Table 2 in the columns designated "rat protein" and "human protein" by at least the homology as specified for the respective sequence in Table 2 in the column designated "%homology" and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(ii) the amino acid specified in Table 2 in the columns designated "rat protein" and "human protein";

(c) a polynucleotide which hybridizes under high stringency conditions to a polynucleotide specified in (a) to (b) and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(d) a polynucleotide the nucleic acid sequence or which deviates from the nucleic acid sequences specified in (a) to (c) due to the degeneration of the genetic code and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(e) a polynucleotide which represents a fragment, derivative or allelic variation of a nucleic acid sequence specified in (a) to (d) and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier".

3. A host cell comprising the vector of claim 2.

4. A method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain, comprising:

(a) hybridizing a nucleic acid sample corresponding to RNA obtained from said animal to a nucleic acid sample comprising one or more nucleic acid molecules of known identity;

(b) measuring the hybridization of said nucleic acid sample to said one or more nucleic acid molecules of known identity, wherein a 1.4 fold difference in the hybridization of said nucleic acid sample to said one or more nucleic acid molecules of known identity relative to a nucleic acid sample obtained from an animal which has not been subjected to said pain is indicative of the differential expression of said nucleotide sequence in said animal subjected to pain.

5. A method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain, comprising:

(a) hybridizing a nucleic acid sample corresponding to RNA obtained from an animal which has been subjected to pain to an array comprising a solid substrate and a plurality of nucleic acid members;

(b) wherein each nucleic acid member has a unique position and is stably associated with the solid substrate;

(c) measuring the hybridization of said nucleic acid sample to said array, wherein a 1.4 fold difference in the hybridization of said nucleic acid sample to one or more nucleic acid members comprising said array relative to a nucleic acid sample obtained from an animal which has not been subjected to said pain is indicative of the differential expression of said nucleotide sequence in said animal subjected to pain.

6. The method of claim 5, wherein a 2 fold change in the hybridization of said nucleic acid sample to one or more nucleic acid members comprising said array relative to a nucleic acid sample obtained from an animal which has not been subjected to said pain is indicative of the differential expression of said nucleotide sequence following pain.

7. A kit for performing any of the methods of claim 4 to 5.

8. An array comprising:

(a) a plurality of polynucleotide members, wherein each of said plurality of polynucleotides is selected from the group consisting of:

(i) a polynucleotide comprising any of the polynucleotides specified in Table 1-2 in the columns designated "rat gene" and "human gene", and wherein at least one of said two or more isolated polynucleotides is unique to Table 2 in the columns designated "rat gene" and "human gene";

(ii) a polynucleotide encoding an amino acid sequence selected from the group consisting of:

(1) amino acid sequences which are homologue to any of the amino acid specified in Table 2 in the columns designated "rat protein" and "human protein" by at least the homology as specified for the respective sequence in Table 2 in the column designated "%homology" and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(2) the amino acid specified in Table 2 in the columns designated "rat protein" and "human protein";

(iii) a polynucleotide which hybridizes under high stringency conditions to a polynucleotide specified in (i) to (ii) and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(iv) a polynucleotide the nucleic acid sequence or which deviates from the nucleic acid sequences specified in (i) to (iii) due to the degeneration of the genetic code and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(v) a polynucleotide which represents a fragment, derivative or allelic variation of a nucleic acid sequence specified in (i) to (iv) and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier"; and

(b) a solid substrate, wherein each polynucleotide member has a unique position on said array and is stably associated with said solid substrate.

9. A method of identifying an agent that increases or decreases the expression of a polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal which is subjected to pain comprising:

(a) administering said agent to said first animal;

(b) hybridizing nucleic acid isolated from one or more sensory neurons of said first and a second animal to the array of claim 8; and

(c) measuring the hybridization of said nucleic acid isolated from said neuronal tissue of said first and second animal to said array; wherein an increase in hybridization of said nucleic acid from said first animal to one or more nucleic acid members of said array relative to hybridization of said nucleic acid from a second animal which is subjected to pain but to which is not administered said agent to one or more nucleic acid members of said array identifies said agent as increasing the expression of said polynucleotide sequence, and wherein a decrease in hybridization of said nucleic acid from said first animal to one or more nucleic acid members of said array relative to the hybridization of said nucleic acid from second animal to one or more nucleic acid members of said array identifies said agent as decreasing the expression of said polynucleotide sequence.

10. A method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, comprising:

(a) providing a cell comprising and capable of expressing one or more of the polynucleotide selected from the group consisting of:

(i) a polynucleotide comprising any of the polynucleotides specified in Table 1-2 in the columns designated "rat gene" and "human gene", and wherein at least one of said two or more isolated polynucleotides is unique to Table 2 in the columns designated "rat gene" and "human gene";

(ii) a polynucleotide encoding an amino acid sequence selected from the group consisting of:

(1) amino acid sequences which are homologue to any of the amino

the homology as specified for the respective sequence in Table 2 in the column designated "%homology" and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(2) the amino acid specified in Table 2 in the columns designated "rat protein" and "human protein";

(iii) a polynucleotide which hybridizes under high stringency conditions to a polynucleotide specified in (a) to (b) and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(iv) a polynucleotide the nucleic acid sequence or which deviates from the nucleic acid sequences specified in (a) to (c) due to the degeneration of the genetic code and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(v) a polynucleotide which represents a fragment, derivative or allelic variation of a nucleic acid sequence specified in (a) to (d) and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(b) contacting said cell with a candidate compound; and

(c) measuring the expression of said one or more of the polynucleotide specified supra, wherein if the expression of said differentially expressed polynucleotide sequence is increased in an animal which is subjected to pain, then said candidate modulator will be considered to regulate the expression of said polynucleotide if the expression of said polynucleotide is decreased by at least 10% in the presence of said candidate modulator, and wherein if the expression of said differentially expressed polynucleotide sequence is decreased in an animal subjected to pain, then said candidate modulator will be considered to regulate the expression of said polynucleotide if the expression of said polynucleotide is increased by at least 10% in the presence of said candidate modulator.

11. A method for identifying a compound which can regulate the activity of one or more of the polypeptides shown in Table 1 or 2, comprising:

(a) providing a cell comprising said one or more polypeptides which are encoded by a polynucleotide selected from the group consisting of:

(i) a polynucleotide comprising any of the polynucleotides specified in Table 1-2 in the columns designated "rat gene" and "human gene", and wherein at least one of said two or more isolated polynucleotides is unique to Table 2 in the columns designated "rat gene" and "human gene";

(ii) a polynucleotide encoding an amino acid sequence selected from the group consisting of:

(1) amino acid sequences which are homologue to any of the amino acid specified in Table 2 in the columns designated "rat protein" and "human protein" by at least the homology as specified for the respective sequence in Table 2 in the column designated "%homology" and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(2) the amino acid specified in Table 2 in the columns designated "rat protein" and "human protein";

(iii) a polynucleotide which hybridizes under high stringency conditions to a polynucleotide specified in (a) to (b) and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(iv) a polynucleotide the nucleic acid sequence or which deviates from the nucleic acid sequences specified in (a) to (c) due to the degeneration of the genetic code and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

a polynucleotide which represents a fragment, derivative or allelic variation of a nucleic acid sequence specified in (a) to (d) and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(b) contacting said cell with a candidate compound; and

(c) measuring the activity of said one or more polypeptides, wherein an increase or decrease of the activity of said one or more polypeptides of at least 10% relative to the activity of

compound, identifies said candidate compound as a compound which regulates the activity of said one or more polypeptides.

12. A method for producing a pharmaceutical formulation comprising:

(a) providing a cell comprising said one or more polypeptides encoded by a polynucleotide selected from the group consisting of:

(i) a polynucleotide comprising any of the polynucleotides specified in Table 1-2 in the columns designated "rat gene" and "human gene", and wherein at least one of said two or more isolated polynucleotides is unique to Table 2 in the columns designated "rat gene" and "human gene";

(ii) a polynucleotide encoding an amino acid sequence selected from the group consisting of:

(1) amino acid sequences which are homologue to any of the amino acid specified in Table 2 in the columns designated "rat protein" and "human protein" by at least the homology as specified for the respective sequence in Table 2 in the column designated "%homology" and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(2) the amino acid specified in Table 2 in the columns designated "rat protein" and "human protein";

(iii) a polynucleotide which hybridizes under high stringency conditions to a polynucleotide specified in (a) to (b) and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(iv) a polynucleotide the nucleic acid sequence or which deviates from the nucleic acid sequences specified in (a) to (c) due to the degeneration of the genetic code and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(v) a polynucleotide which represents a fragment, derivative or allelic variation of a nucleic acid sequence specified in (a) to (d) and encodes a polypeptide exhibiting

the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(b) selecting a compound which regulates the activity of said one or more polypeptides; and

(c) mixing said compound with a carrier.

13. The method of claim 12, wherein said step of selecting comprises the steps of

(a) contacting said cell with a candidate compound; and

(b) measuring the activity of said one or more polypeptides, wherein an increase or decrease of the activity of said one or more polypeptides of at least 10% relative to the activity of said one or more polypeptides in said cell, wherein the cell is not contacted with the candidate compound, identifies said candidate compound as a compound which regulates the activity of said one or more polypeptides

14. A method for identifying a compound which can regulate the activity, in an animal, of one or more of the polypeptides shown in Table 2, comprising:

(a) administering a candidate compound to an animal comprising said one or more polypeptides, or a unique fragment therefrom exhibiting the activity of ....; and

(b) measuring the activity of said one or more polypeptides wherein an increase or decrease of the activity of said polypeptide of at least 10% relative to the activity of said one or more polypeptides in an animal to which the candidate compound is not administered, identifies said candidate compound as a compound which regulates the activity of said one or more polypeptides.

15. A method for identifying a small molecule which regulates the activity of one or more of the polypeptides indicated in Table 2, comprising:

(a) providing a cell comprising said one or more polypeptides encoded by a polynucleotide selected from the group consisting of:

(i) a polynucleotide comprising any of the polynucleotides specified in Table 1-2 in the columns designated "rat gene" and "human gene", and wherein at least one of said two

or more isolated polynucleotides is unique to Table 2 in the columns designated "rat gene" and "human gene";

(ii) a polynucleotide encoding an amino acid sequence selected from the group consisting of:

(1) amino acid sequences which are homologue to any of the amino acid specified in Table 2 in the columns designated "rat protein" and "human protein" by at least the homology as specified for the respective sequence in Table 2 in the column designated "%homology" and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(2) the amino acid specified in Table 2 in the columns designated "rat protein" and "human protein";

(iii) a polynucleotide which hybridizes under high stringency conditions to a polynucleotide specified in (a) to (b) and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(iv) a polynucleotide the nucleic acid sequence or which deviates from the nucleic acid sequences specified in (a) to (c) due to the degeneration of the genetic code and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(v) a polynucleotide which represents a fragment, derivative or allelic variation of a nucleic acid sequence specified in (a) to (d) and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(b) generating a small molecule library;

(c) providing a candidate small molecule, selected from said library;

(d) contacting said cell with said candidate small molecule; and

(e) measuring the activity of said one or more polypeptides, wherein an increase or decrease of the activity of said one or more polypeptides of at least 10% relative to the activity of

small molecule, identifies said candidate small molecule as a small molecule which regulates the activity of said one or more polypeptides.

16. The method of claim 15, wherein said small molecule library comprises components selected from the group consisting of heterocyclics, aromatics, alicyclics, aliphatics, steroids, antibiotics, enzyme inhibitors, ligands, hormones, alkaloids, opioids, terpenes, porphyrins, toxins, and catalysts, and combinations thereof.

17. A method for identifying a compound useful in the treatment of pain, comprising:

(a) providing a host cell comprising a vector comprising one or more of the polynucleotides selected from the group consisting of:

(i) a polynucleotide comprising any of the polynucleotides specified in Table 1-2 in the columns designated "rat gene" and "human gene", and wherein at least one of said two or more isolated polynucleotides is unique to Table 2 in the columns designated "rat gene" and "human gene";

(ii) a polynucleotide encoding an amino acid sequence selected from the group consisting of:

(1) amino acid sequences which are homologue to any of the amino acid specified in Table 2 in the columns designated "rat protein" and "human protein" by at least the homology as specified for the respective sequence in Table 2 in the column designated "%homology" and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(2) the amino acid specified in Table 2 in the columns designated "rat protein" and "human protein";

(iii) a polynucleotide which hybridizes under high stringency conditions to a polynucleotide specified in (a) to (b) and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(iv) a polynucleotide the nucleic acid sequence or which deviates from the nucleic acid sequences specified in (a) to (c) due to the degeneration of the genetic code and

encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(v) a polynucleotide which represents a fragment, derivative or allelic variation of a nucleic acid sequence specified in (a) to (d) and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(b) maintaining said host cell under conditions which permit the expression of said one or more polynucleotides;

(c) selecting a compound which regulates the activity of a polypeptide encoded by said one or more polynucleotides;

(d) administering said compound to an animal subjected to pain; and

(e) measuring the level of pain in said animal, wherein a decrease in the level of pain in said animal of at least 10%, identifies said compound as being useful for treating pain.

18. The method of claim 17, wherein said step of selecting includes the steps of

(a) contacting said cell with a candidate compound; and

(b) measuring the activity of the polypeptide encoded by said one or more polynucleotides, wherein an increase or decrease of the activity of said polypeptide of at least 10% relative to the activity of said polypeptide in said cell, wherein the cell is not contacted with the candidate compound, identifies said candidate compound as a compound which regulates the activity of said polypeptide.

19. The use of a compound identifiable by any of the methods of claim 9 to 17 in the preparation of a medicament for the treatment of pain in an animal.

20. The use of:

(a) a polynucleotide selected from the group consisting of:

(i) a polynucleotide comprising any of the polynucleotides specified in Table 1-2 in the columns designated "rat gene" and "human gene", and wherein at least one of said two

or more isolated polynucleotides is unique to Table 2 in the columns designated "rat gene" and "human gene";

(ii) a polynucleotide encoding an amino acid sequence selected from the group consisting of:

(1) amino acid sequences which are homologue to any of the amino acid specified in Table 2 in the columns designated "rat protein" and "human protein" by at least the homology as specified for the respective sequence in Table 2 in the column designated "%homology" and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(2) the amino acid specified in Table 2 in the columns designated "rat protein" and "human protein";

(iii) a polynucleotide which hybridizes under high stringency conditions to a polynucleotide specified in (a) to (b) and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(iv) a polynucleotide the nucleic acid sequence or which deviates from the nucleic acid sequences specified in (a) to (c) due to the degeneration of the genetic code and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(v) a polynucleotide which represents a fragment, derivative or allelic variation of a nucleic acid sequence specified in (a) to (d) and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(vi) a polypeptide encoded by any of the polynucleotides specified in (i) to (v);

in the preparation of a medicament for the treatment of pain in an animal.

21. The use of a compound which can modulate the activity of a polypeptide which is encoded by a polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising any of the polynucleotides specified in Table 1-2 in

more isolated polynucleotides is unique to Table 2 in the columns designated "rat gene" and "human gene";

(b) a polynucleotide encoding an amino acid sequence selected from the group consisting of:

(i) amino acid sequences which are homologue to any of the amino acid specified in Table 2 in the columns designated "rat protein" and "human protein" by at least the homology as specified for the respective sequence in Table 2 in the column designated "%homology" and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(ii) the amino acid specified in Table 2 in the columns designated "rat protein" and "human protein";

(c) a polynucleotide which hybridizes under high stringency conditions to a polynucleotide specified in (a) to (b) and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(d) a polynucleotide the nucleic acid sequence or which deviates from the nucleic acid sequences specified in (a) to (c) due to the degeneration of the genetic code and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(e) a polynucleotide which represents a fragment, derivative or allelic variation of a nucleic acid sequence specified in (a) to (d) and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

in the preparation of a medicament for the treatment of pain in an animal.

22. A pharmaceutical formulation comprising one or more polypeptides encoded by a polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising any of the polynucleotides specified in Table 1-2 in the columns designated "rat gene" and "human gene", and wherein at least one of said two or more isolated polynucleotides is unique to Table 2 in the columns designated "rat gene" and "human gene";

(b) a polynucleotide encoding an amino acid sequence selected from the group consisting of:

(i) amino acid sequences which are homologue to any of the amino acid specified in Table 2 in the columns designated "rat protein" and "human protein" by at least the homology as specified for the respective sequence in Table 2 in the column designated "%homology" and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(ii) the amino acid specified in Table 2 in the columns designated "rat protein" and "human protein";

(c) a polynucleotide which hybridizes under high stringency conditions to a polynucleotide specified in (a) to (b) and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(d) a polynucleotide the nucleic acid sequence or which deviates from the nucleic acid sequences specified in (a) to (c) due to the degeneration of the genetic code and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(e) a polynucleotide which represents a fragment, derivative or allelic variation of a nucleic acid sequence specified in (a) to (d) and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

and a carrier.

23. A pharmaceutical formulation comprising one or more antibodies which bind to one or more of the polypeptides encoded by a polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising any of the polynucleotides specified in Table 1-2 in the columns designated "rat gene" and "human gene", and wherein at least one of said two or more isolated polynucleotides is unique to Table 2 in the columns designated "rat gene" and "human gene";

(b) a polynucleotide encoding an amino acid sequence selected from the group

(i) amino acid sequences which are homologue to any of the amino acid specified in Table 2 in the columns designated "rat protein" and "human protein" by at least the homology as specified for the respective sequence in Table 2 in the column designated "%homology" and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(ii) the amino acid specified in Table 2 in the columns designated "rat protein" and "human protein";

(c) a polynucleotide which hybridizes under high stringency conditions to a polynucleotide specified in (a) to (b) and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

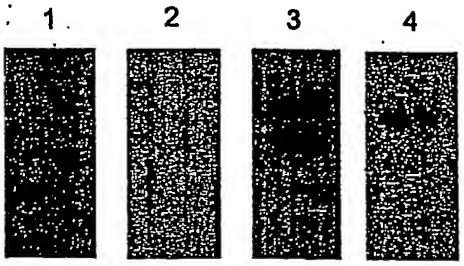
(d) a polynucleotide the nucleic acid sequence or which deviates from the nucleic acid sequences specified in (a) to (c) due to the degeneration of the genetic code and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

(e) a polynucleotide which represents a fragment, derivative or allelic variation of a nucleic acid sequence specified in (a) to (d) and encodes a polypeptide exhibiting the biological function as specified for the respective sequence in Table 2 in the column designated "identifier";

and a carrier.

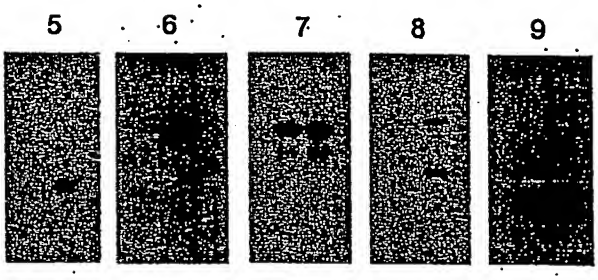
Figure 1

Ax <1000

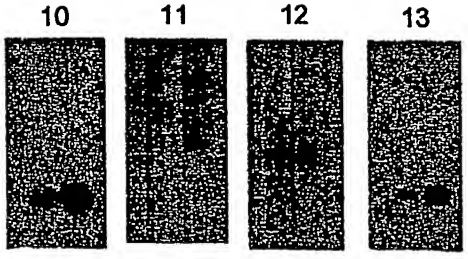


	53 Kd	CCK-B	Enk	ET-B
Level (Axotomy)	884	934	647	705
Affymetrix Ratio	2.4	3	1.9	1.2

1000< Ax <5000

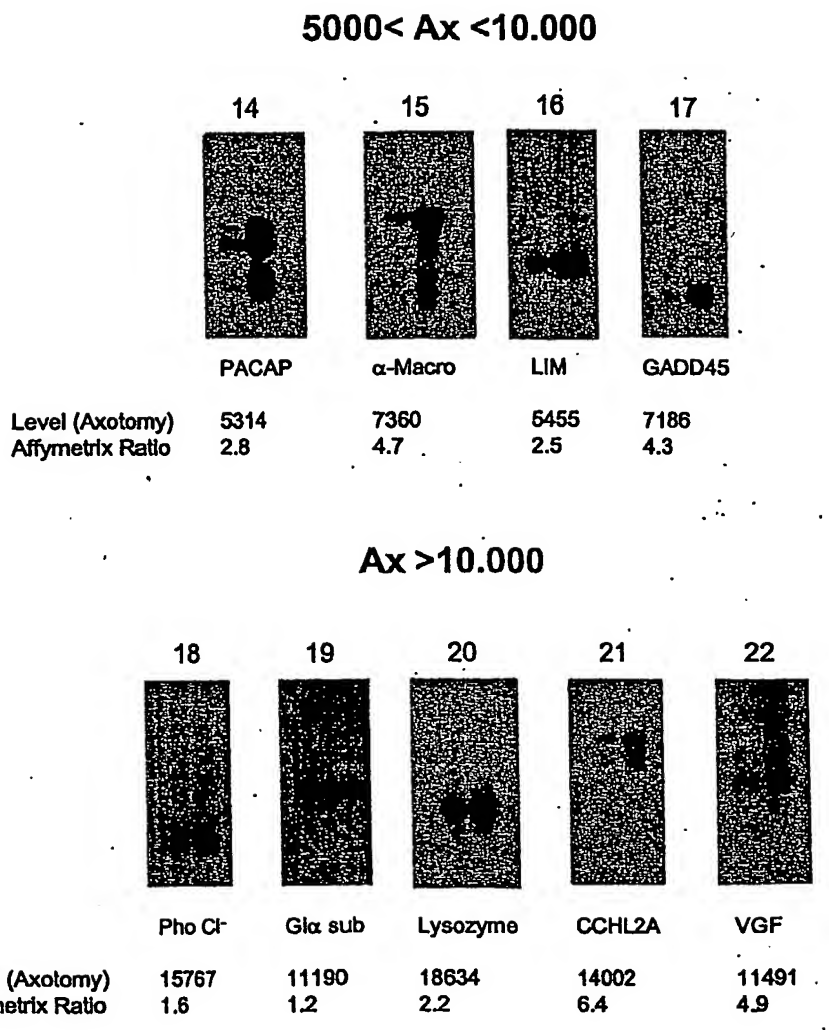


	SProR	GTPcyclo	MSS4	GFRα1	PKBS
Level (Axotomy)	3566	1099	1980	3835	1813
Affymetrix Ratio	4	5.4	1.1	2.5	1.8



	MET-1	Endo-1	Forkhead	JE IE
Level (Axotomy)	2383	1188	3438	4902
Affymetrix Ratio	4	3.7	1.3	3.2

Figure 1 Continued



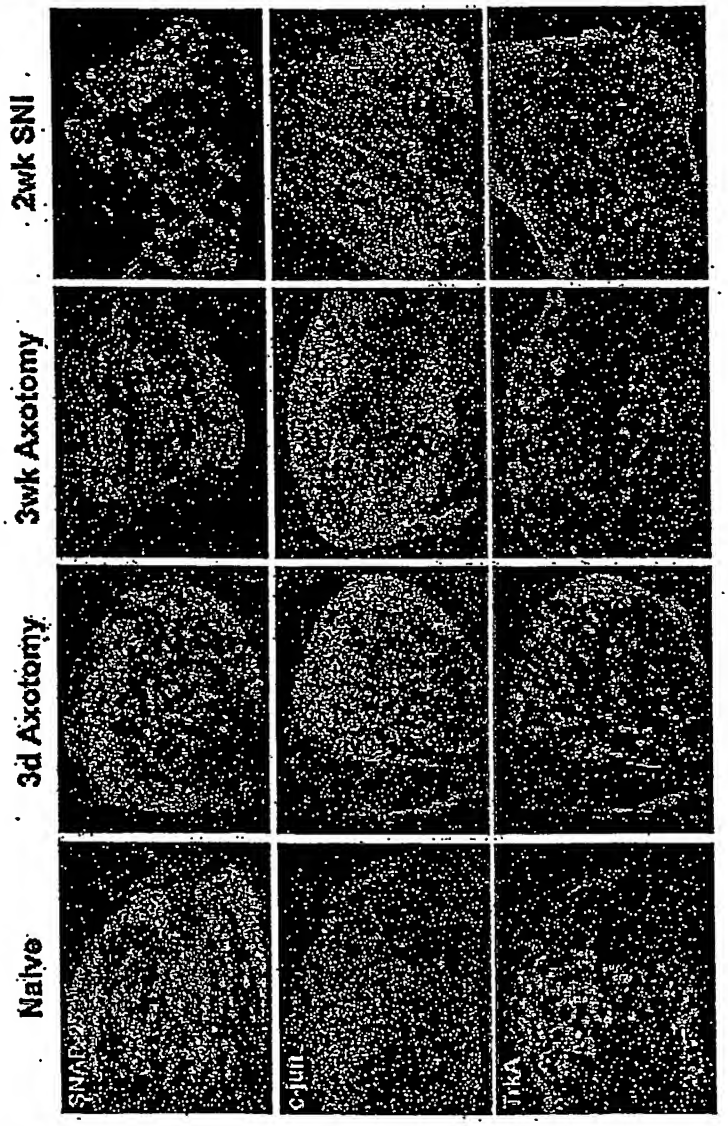


Figure 2

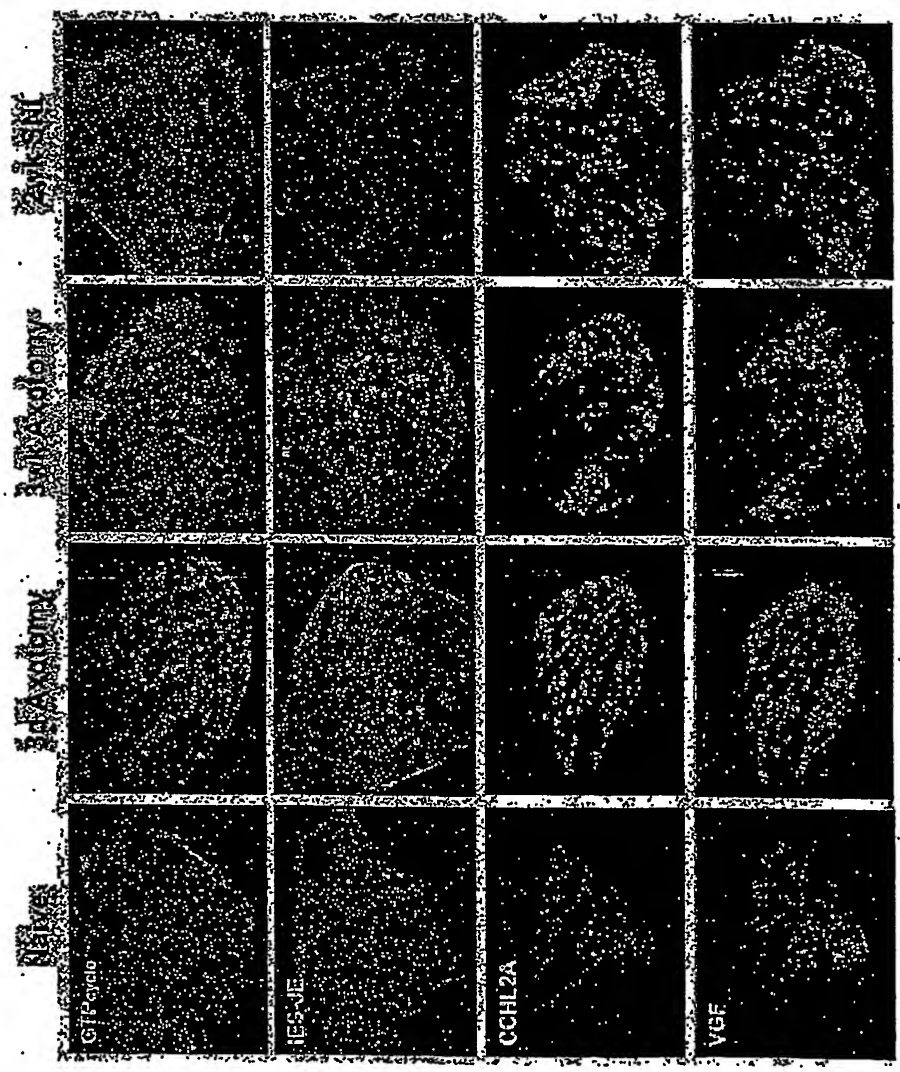


Figure 3